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OM protein - protein search, using sw model

Run on:

3, 2005, 15:29:50 ; Search time 151 Seconds January

(without alignments)
23.757 Million cell updates/sec

1 cgywltiwgc 10 Perfect score: Sequence:

SEQ33

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2002273 seqs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_23Sep04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

•		ap.				
Result No.	Score	Ouery Match	Query Match Length DB	DB	OI OI	Description
7	72	100.0	10	ß	ABP53932	Abp53932 VEGFR-3 b
~	54	75.0	10	S	ABP53931	Abp53931 VEGFR-3 b
m	20	69.4	10	ß	ABP53968	Abp53968 VEGFR-3 b
4	47.5	0.99	304	7	ADC87481	Adc87481 Human GPC
ហ	47	65.3	25	7	ADC99638	Adc99638 Cancer-re
9	46	63.9	17	9	AA026074	Aao26074 Fc region
7	46	63.9	17	ω	ADJ50741	Adj50741 Human ser
80	46	63.9	136	ω	ADM87650	Adm87650 Human EST
0	45	62.5	20	Ŋ	AAU90545	Aau90545 Insulin/1
10	45	62.5	129	N	AAY59880	Aay59880 Human nor
11	45	62.5	828	9	ABU49938	Abu49938 Protein e
12	44.5	61.8	1024	S	ABB04861	Abb04861 LDL recep
13	44	61.1	149	8	ADP29850	Adp29850 Human sec
14	44	61.1	166	9	AAE31487	Aae31487 Human but
15	44	61.1	415	Ŋ	AAU91293	Aau91293 Human NOV
16	43	59.7	13	9	AA026093	Aao26093 Fc region
17	43	59.7	13	œ	ADJ50760	
18	43	59.7	454	ហ	ABP73979	
19	43	59.7	474	9	ABU3 0 0 0 4	Abu30004 Protein e
20	43	59.7	492	7	ADC97318	Adc97318 E. faeciu
21	43	59.7	1084	Φ.	ADL81869	Adl81869 P. aerugi
22	42.5	59.0	152	m	AAY94989	Aay94989 Human sec
23	42.5	59.0	152	Ŋ	ABB90081	Abb90081 Human pol
24	42.5	59.0	152	ហ	AA017173	Aao17173 Human sec
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Adl78051 Albumin f Aar66278 Therapeut Aab12156 Hydrophob		Abg64785 Human alb Adl78052 Albumin f Adn05188 Antipsori	Abb12006 Human gli		Rat	Aab20122 Rat sodiu Aab20123 Rat sodiu Add32192 Rat Na v
ADL78051 AAR66278 AAB12156	AAM78581 AAB73100 AAO17198	ABG64785 ADL78052 ADN05188	AAM25822 ABB12006 AAM79565	AB007116 ABB04863 AAX16572	AAY41668 AAY06596	AAB20122 AAB20123 ADD32192
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4 4 4 2 2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	4 4 4 2 2 . 5 2 . 5 . 5 . 5 . 5 . 5 . 5 . 5 .	4.4.4.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2	24.4 22.5 2.5 2.5 2.5	4 4 4 4 6 6 6 6 6 6 6 6 6 6 6	42.5	4 4 4 2 2 5 4 4 2 2 5 5 5 5 5 5 5 5 5 5
26 27 28	30 31	33 34 34	35	2 E E 4	4 4 2 2	4 4 4 5 4 5

ALIGNMENTS

Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypetrension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor. VEGFR-3 binding peptide SEQ ID NO:35. ABP53932 standard; peptide; 10 AA. (first entry) 09-JAN-2003 ABP53932; RESULT 1 **ABP53932**

sapiens. Synthetic.

WO200257299-A2.

25-JUL-2002.

16-JAN-2002; 2002WO-IB000099.

(LUDW-) LUDWIG INST CANCER RES.

17-JAN-2001; 2001US-0262476P.

LICENTIA LTD. (LICN)

Alitalo K, Koivunen E,

Kubo H;

WPI; 2002-691521/74.

New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.

Claim 13; Page 80; 149pp; English

The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGRR-3). (I) have cytostatic, hepatorropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

Abg64784 Human alb

5 ABG64784

152

59.0

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vascular endothelial growth factor receptor 3 inhibitor; VBGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antiidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
                      ovary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endomerrium, prostate, testicle, ovary skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                          100.0%; Score 72; DB 5; Length 10; 100.0%; Pred. No. 0.0025; cive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEGFR-3 binding peptide SEQ ID NO:34.
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                                                                                                                                                                                                                                                                                                                                                                          ABP53931 standard; peptide; 10 AA
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                                                                                                                                                                                                               10; Conservative
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                                                                                                                                                                                               Best Local Similarity
                                                                                                          present invention
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                                                                                                                                           Sequence 10 AA;
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                                                                                                                                                                              Query Match
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ABP53931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypetrension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
               ovary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
          pancreas, colon, stomach, breast, endometrium, prostate, testicle, ov
skin, head and neck, oesophagus, bone, marrow or blood, and diseases
neovascularisation, e.g. liver diseases, hypertension, post-trauma,
chronic hepatitis, haemangiomas and diabetes. The present sequence
represents a specifically claimed VEGFR-3 binding peptide from the
present invention
                                                                                                                                                                                                Gaps
liver, spleen, kidney, lymph node, small intestine, blood cells,
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0.67;
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                                                                                                                                                                          100.0%; Prec. ...
                                                                                                                                                               75.0%; Score 54; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 ABP53968 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                             Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                 Sequence 10 AA;
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ABP53968
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Cancer-related Tie-1-binder peptide - SEQ ID 476.

(first entry)

01-JAN-2004

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ADC99638 standard; peptide; 25

RESULT 5 ADC99638

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                          pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemanglomas and diabetes. The present sequence represents a VEGFR-3 binding peptide, which is given in the exemplification of the present invention
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spleen, kidney, lymph node, small intestine, blood cells,
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(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
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Pred. No. 2.3;
0; Mismatches
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Best Local Similarity 60.v
                                                                                                                                                                                                                                                                                                                                                                                  6, Conservative
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Best Local Similarity
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ADC874
88888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Selecting target and target binder pairs for preparing a composition for treating cancer by mixing in a reaction vessel phage expressing biological targets and phage expressing target binders.
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                                                                                                                  cytostatic, cancer; gene therapy; DGI-2; DGI-5; DGI-7; DGI-9; Hras; leptin; VEGF; vascular endothelial growth factor receptor; VEGF-R1; VEGF-R2; VEGF-R3; PMS-related tyrosine kinase 1; FLK1; KDR; Kinase insert domain protein receptor; EGFR; epidermal growth factor; FGFR1; fibroblast growth factor; Tie-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 26; SEQ ID NO 476; 172pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                       Spruyt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAO26074 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                        (DGIB-) DGI BIOTECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                           24-OCT-2002; 2002WO-US034021.
                                                                                                                                                                                                                                                                                                                                         24-OCT-2001; 2001US-0345471P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                     Goldstein N;
                                                                                                                                                                                                                                                                                                                                                                                                       Brissette R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-457332/43.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     Prendergast J,
                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                       Pillutla RC,
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108 CGFW-AVWGC 116

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1 CGYWLTIWGC 10

seq33.rag

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21-JUL-2001; 2001US-0306971P.
28-MAR-2002; 2002US-00112944.
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                                                                                                                                                                                                                                                                                                              63.9%;
66.7%;
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Ghosh MJ, Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                     6; Conservative
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4 CGFWPRIWG 12
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 WPI; 2004-082161/08.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                             1 CGYWLTIWG
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                                                                                                                                                                                                                                                                                       Sequence 17 AA;
                                                            and evaluated
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                       Evaluating s
comprising s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADM87650;
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                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
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                                                                                                                                                                                                                            New polypeptides, useful as binding molecules for detecting, isolating or purifying immunoglobulin Fc-region polypeptides present in a solution, or for regulating or preventing an antibody response.
                                                                                                                                                                                                                                                                                               The invention relates to novel isolated polypeptides comprising a sequence that binds an immunoglobulin Fc region. The polypeptides are useful as binding molecules for detecting, isolating or purifying immunoglobulin Fc-region polypeptides present in a solution, e.g. blood, plasma or transgenic milk. The Fc-region binding polypeptides are also useful for regulating or preventing an antibody response, or for increasing the half-life and over all stability of a therapeutic or diagnostic compound that is administered to or enters the circulatory system of an individual. This sequence represents an Fc region binding
Immunoglobulin Fc region; binding; whole blood; plasma; transgenic milk;
antibody response; half-life; stability; circulatory system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                               Potter MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46; DB 6; Length 17;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human serum albumin; HSA; serum; blood; tumour; human.
                                                                                                                                                                               Ransohoff TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human serum albumin binding peptide, Seq ID No 278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                               Stochl M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ50741 standard; peptide; 17 AA
                                                                                                                                                                                                                                                                            Claim 3; Page 76; 152pp; English
                                                                                                         18-APR-2002; 2002WO-US012492.
                                                                                                                                18-APR-2001; 2001US-0284534P
                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.9%;
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                                                                                                                                                                               Ley AC,
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                                                                                                                                                                                                                                                                                                                                                                                                           of the invention
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CGFWPRIWG 12
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                                                                                                                                                                                                     WPI; 2003-201220/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
ses 6, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CGYWLTIWG
                                                                                                                                                       (DYAX-) DYAX CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003106493-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 AA;
                                                          WO200286070-A2
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                                  Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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The invention relates to a method of evaluating sample by providing a soluble serum protein (I), one or more compounds physically associated with (I), and a (I)-binding agent that comprises a peptide that especifically binds to (I), allowing the (I)-binding agent to bind to (I) to form a complex including one or more compounds physically associated with (I), separating the complex from one or more components of the sample, and evaluating one or more of the physically associated compounds. The sample comprises blood or serum, or is obtained from a biopsy. The sample may also be obtained from a tumour or a region within 5 mm of a tumour. The method is useful for detecting modulators that modulate interaction of serum protein-binding compound and serum protein sequence represents a serum albumin-binding peptide identified using the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
Evaluating sample comprising soluble serum protein by forming complex comprising serum protein and physically associated compounds using peptide ligand that specifically binds with proteins, which is separated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              respiratory; cytostatic; antiarthritic; antiinflammatory; gastrointestinal; antibacterial; immunosuppressive; antidiabetic; antirheumatic; gene therapy; molecular weight marker; chromosome marker; chromosome tag; genetic fingerprinting; nutritional supplement; cancer; inflammatory condition; arthritis; inflammatory bowel disease; crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1; graft versus host disease; human; expressed sequence tag; EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotides and polypeptides, useful for treating, e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     À,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ren F, Xue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                   Disclosure; SEQ ID NO 278; 191pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang J, Ren
D, Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADM87650 standard; protein; 136 AA.
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The present invention describes an isolated polymuclectide (I): (a)

comprising a nuclectide sequence selected from SEQ ID NO:1-244; or (b)

which encodes a polypeptide with biological activity, where the

polymuclectide hybridises to (I) under stringent hybridisation conditions

or has greater than 99% sequence identity with (I). (I) has respiratory,

cytostatic, antiarthritic, antiinflammatory, gastrointestinal,

cytostatic, antiarthritic, antiinflammatory, gastrointestinal,

cytostatic, antiarthritic, antiinflammatory, gastrointestinal,

cytostatic, and can be used in gene therapy. (I) can be used for

generating polymucleotides encoding chimeric or fusion proteins and

cativities, and can be used in gene therapy. (I) can be used to

generating polymucleotides encoding chimeric or fusion proteins and

cativities, and can be used in which the corresponding protein is

preferroinally expressed; as molecular weight markers on gels; as

chromosome markers or tags to identify chromosomes or to map related gene

continons; to compare with endogenous DNA sequences or to map related gene

continons; to compare with endogenous DNA sequences in patients to

dentify potential genetic disorders; as probe to subtract-out known

con genes, related DNA sequences; as probe to subtract-out known

sequences in the process of discovering other novel polymucleotides; for

selecting and making oligeners for attachment to a gene chip or other

compositions and polypeptides can also be used as nutritional sources

con supplements, e.g. as a protein or amino acid supplement, as a carbon

source, as a nitrogen source or as a source of carbohydrates. The

polymucleotides and polypeptides can also be used as nutritional

confostitions are useful for promoting better or faster calceur. The

compositions are useful for promoting better or faster closure of nor

healing wounds, for the generation and regeneration of tissues, for generation withing relative or faster closure of proverser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage. The compositions can also be used to treat inflammatory conditions (e.g. arthritis, inflammatory bowel disease or Crohn's disease), sepsis, rheumatorid arthritis, diabetes mellitus type 1 or graft versus host disease. The present sequence represents an expressed sequence tag (EST) derived amino acid sequence from the present
cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease,
Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention. N.B. The sequences for this patent were obtained from the USPTO web site from an equivalent US patent US20040048249A1.
                                                                                                                                              Example 2; SEQ ID NO 743; 591pp; English
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Sequence 136 AA;

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Gaps
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          Score 46; DB 8; Length 136; Pred. No. 73;
                                3; Indels
                               1; Mismatches
         63.9%;
60.0%;
Query Match
Best Local Similarity 60..
Best 6; Conservative
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1 CGYWLTIWGC 10

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93 CGRWDWLWGC 102

RESULT 9 AAU90545

AAU90545 standard; peptide; 20 AA

Human; uterus; cancer; treatment; anticancer; cytostatic; gene therapy; EST; expressed sequence tag.

Human normal uterus tissue derived protein 43.

19-JAN-2000 (first entry)

AAY59880;

AAY59880 standard; protein; 129 AA.

RESULT 10 AAY59880

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18-JUN-2002 (first entry)

AAU90545;

Insulin/insulin-like growth factor receptor-binding peptide #2501

Cytostatic; antidiabetic; neuroprotective; cerebroprotective; ophthalmological; insullin; receptor; gene therapy, diabetes; insullin-like growth factor-1; IGP-1; tumour; prostate; breast; diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.

(META-) METAGEN GES GENOMFORSCHUNG MBH.

17-APR-1998;

98DE-01017946. 98DE-01017946

17-APR-1998; 21-OCT-1999.

DE19817946-A1

Homo sapiens.

Synthetic

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The invention relates to a method of modulating insulin activity in mammalian cells by administering a peptide that binds the insulin receptor (IR). A composition containing a peptide, optionally expressed from gene therapy vectors, that binds to Site 1 of IR and an insulin agonist are useful for treating diabetes. Also, peptides that are antagonists of the insulin-like growth factor (IGP-1) receptor are useful for treating insulin-like growth factor (IGP-1) receptor are useful for treating insulin-like growth factor (IGP-1) receptor treating insulin-like growth factor (IGP-1) receptor are useful for treating neurological diseases, including stroke and diabetic neuropsthy. The peptides are also useful in therapeutics and research reagents. ANU88034-AAU90957 represent IR and/or IGP-1 receptor-binding peptides and related amino acid sequences of the
                                                                                                                                                                                                                                                                                              Modulating insulin activity in mammalian cells, for treating e.g. diabetes and tumors, comprises using peptides that bind to insulin or insulin-like growth factor receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                         Pillutla R, Brandt J;
Ostergaard S, Mandecki WS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred. No. 20;
0; Mismatches 4; Indels
                                                                                                                                                                                         Schaeffer L,
J, Cheng W,
Hsiao K,
                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 8-3; 390pp; English.
                                                                                                                                      (DGIB-) DGI BIOTECHNOLOGIES LLC (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.5%;
60.0%;
                                                                    29-MAR-2000; 2000WO-US008528.
                                                                                                   29-MAR-2000; 2000WO-US008528
                                                                                                                                                                                                            Spetzler J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
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                                                                                                                                                                                                          Brissette R, Spetzler
Hansen PH, Ravera M,
                                                                                                                                                                                                                                                             WPI; 2002-025774/03.
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 AA;
WO200172771-A2
                                  04-OCT-2001
                                                                                                                                                                                           Beasley J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention
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Tue Jan

This invention describes novel cDNA sequences (A) highly expressed in normal uterine tissue which can have anticancer and cytostatic activity and can be used for gene therapy. (A) are used (1) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of uterine cancer; (ii) directly for treating this form of cancer (including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling ESTB (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTB from different libraries may represent different parts of the same curknown gene, distorting the estimated frequency of cocurrence in a particular tissue. ANYS9838-X5983 represent protein fragments encoded by the human uterine tissue derived CDNA fragments represented in AAZ41325-New nucleic acid sequences expressed in normal uterine tissues, and derived polypeptides, for treatment of uterine cancer and identification Antisense; prokaryotic essential gene; cell proliferation; drug design. ы Н Zyskind JW; Xu HH; Gaps Dahl ö Schmitt A, Pilarsky C, 62.5%; Score 45; DB 2; Length 129; 62.5%; Pred. No. 96; 1; Indels tive 2; Mismatches 1; Indels Ohlsen KL, Forsyth RA, Protein encoded by Prokaryotic essential gene #35465. Haselbeck R, Yamamoto R, Hinzmann B, ABU49938 standard; protein; 828 AA. Claim 23; Page 138; 154pp; German. Malone C, Carr GJ, 06-SEP-2001; 2001US-00948993. 25-0CT-2001; 2001US-0342923P. 06-FEB-2002; 2002US-0072851. 06-MAR-2002; 2002US-036289P. 21-MAR-2001; 2001US-00815242. 21-MAR-2002; 2002WO-US009107 (first entry) (ELIT-) ELITRA PHARM INC. Local Similarity 62.5 nes 5; Conservative Specht T, therapeutic agents. | :|||:| CSHWLTVW 39 Zamudio C, Trawick JD, WPI; 1999-591956/51. 1 CGYWLTIW 8 WPI; 2003-029926/02. N-PSDB; ACA53808. Sequence 129 AA; N-PSDB; AAZ41339 rersinia pestis. WO200277183-A2. Rosenthal A, 19-JUN-2003 03-OCT-2002. ABU49938; Query Match Wang L, Wall D, RESULT 11 ABU49938 Matches 8 ઠે

the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid conciding a polypeptide whose expression is inhibited by the antisense conciding a polypeptide whose expression is inhibited by the antisense conciding a polypeptide whose expression is inhibited by the antisense contisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the contisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway concluded for the gene product or that has an activity against a biological pathway concluded for proliferation or that inhibits cellular proliferation; (8) identifying a compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling the extent or organism acts; (9) manufacturing an antibiotic; (10) profiling the extent organism; or (11) identifying the target of a compound that inhibits the proliferation of an organism. The attisense nucleic acids are useful for proliferation of an organism. The antisense nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, concluding discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, concludent dincettyly from MIPO at the printed specification, but was obtained for the print of the printed specification, but was obtained for the print of the printed specification, but with any or the same according the concluding the concluding and proper security of the printed specification, but with any or the same according the same according the same according the same according the same accor 1; New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. The invention relates to an isolated nucleic acid comprising any one of Low density lipoprotein receptor binding protein; signal transduction; LDL receptor binding protein; LDL receptor signalling pathway. Gaps 5 LDL receptor binding protein Na channel brain 3 SEQ ID NO:84 Score 45; DB 6; Length 828; Pred. No. 4.6e+02; 1; Mismatches 2; Indels SEQ ID NO 77862; 1766pp; English. tp.wipo.int/pub/published_pct_sequences ABB04861 standard; protein; 1024 AA. 24-APR-2001; 2001WO-US013214. 62.58; 58.3%; 13-MAR-2002 (first entry) 372 ČĠĽWĽEĽĽSWĠĆ 383 7; Conservative 1 CGYWLTI--WGC 10 Local Similarity Sequence 828 AA; WO200184159-A2. 08-NOV-2001 Synthetic. Claim 25; ABB04861; Query Match Matches RESULT 12 g 8

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01-MAY-2000; 2000US-00562737

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The present invention relates to an isolated nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1848; 428pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JUL-2003;
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  The present invention describes a method for detecting a stress that alters a functional interaction of a low density lipoprotein (LDL) receptor binding protein (I) with an LDL receptor interaction domain (II). The method involves introducing a predetermined stress into a system which provides a stress-biased physical interaction of (I) with circumparts of the stress, the system provides an unbiased interaction of (I) and (II), and detecting the stress-biased interaction of (I) and (II), where a difference between BI and UI indicates that the stress alters the interaction of (I) and (II). (I) is selected from of (I) and (II), where a difference between BI and UI indicates that the stress alters that interaction of (I) in selected from channel brain 3, Mintl, ICAP-1 and APC subunit 10. The method is useful for detecting a stress that alters functional interaction of LDL receptor binding polypeptide with LDL receptor interaction domain. The method is useful for detecting and modulating signal transduction through LDL receptors ABB04778 to ABB04909 represent LDL receptor binding proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
                                                                     Detecting stress that alters interaction of LDL receptor binding polypeptide with LDL receptor interaction domain, comprises detecting difference in stress-biased and unbiased interaction of peptide and
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                 61.8%; Score 44.5; DB 5; Length 1024; 54.5%; Pred. No. 6.5e+02; ive 3; Mismatches 1; Indels 1.
                                                                                                                              Disclosure; Page 148-150; 200pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP29850 standard; protein; 149 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein SEQ ID #617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-AUG-2002; 2002US-0406576P.
29-AUG-2002; 2002US-040658P.
29-AUG-2002; 2002US-040658BP.
29-AUG-2002; 2002US-040658BP.
29-AUG-2002; 2002US-040661BP.
29-AUG-2002; 2002US-040661LP.
29-AUG-2002; 2002US-040661LP.
29-AUG-2002; 2002US-040661CP.
29-AUG-2002; 2002US-040661CP.
29-AUG-2002; 2002US-040664PP.
29-AUG-2002; 2002US-040664CP.
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(TEXA ) UNIV TEXAS SYSTEM
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                       Gotthardt M;
                                             WPI; 2002-082855/11.
                                                                                                         domain in a system.
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                                                                                                                                                                                                                                                                                                                                                             Sequence 1024 AA;
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New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
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2002US-0410957P.
2002US-0410958P.
2002US-0410959P.
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2002US-0410961P.
2002US-0410962P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to B7-H1.2 or Butryophilin 2/3 polypeptides of human B7 polypeptide family and polymucleotides encoding such proteins. Sequences of the invention are useful for treating an immunological conditions (e.g., transplant rejection, graft-versus-host disease, allergy, asthma, inflammatory bowel disease, seppis), diseases that are caused or exacerbated by T-cell mediated inflammation (e.g., Alzheimer's disease or atherosclerosis), autoimmune diseases (e.g., systemic lupus erythematosus, autoimmune diseases (disease, psoriasis, multiple sclerosis, autoimmune diabetes, diabetic neuropathy, theumatoid arthritis), bacterial or viral infections end and immunodeficiency virus (HIV) infection, delayed reconstitution of T-cells, defects in T-
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encoding a polypeptide which is believed to be cytostatic, antifinatiflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
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                                                                                                                                                                                               61.1%; Score 44; DB 8; Length 149; 62.5%; Pred. No. 1.5e+02; ive 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAE31487 standard; protein; 166 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human butryophilin 2/3 protein.
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19-JAN-2001; 2001US-0262737P.
07-JAN-2002; 2002US-00260617.
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1es 5, Conservative
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CHFWLTVW 102
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                                                                                                                                                              Sequence 149 AA;
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y cell function or congenital immunodeficiencies. They gene therapy. The present sequence is human butryophilin
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                                                                                                                                                                                                                                 Gaps
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Patturajan M;
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                                                                                                                                                                      Length 166;
                                                                                                                                                                         Score 44; DB 6; Length 166
Pred. No. 1.6e+02;
1; Mismatches 2; Indels
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Rastelli L, Verney CAM,
Taupier RJ;
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62.5%;
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2000US-0228324P.
2000US-0228997P.
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01-SEP-2000; 2000US-0229848P.
01-SEP-2000; 2000US-0229850P.
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31-JAN-2001; 2001US-0265518P.
15-MAR-2001; 2001US-027641P.
27-MAR-2001; 2001US-0279196P.
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Padigaru M,
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        accessory cell
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Best Local Similarity
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                                                                consensus protein
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                                                                                                                          Sequence 166 AA;
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C The invention relates to an isolated cytoplasmic, nuclear, membrane bound or secreted polypeptide, designated NOVX (actually NOVI, 2a, 2b, 3a, 3b, 4 5a, 5b, 5c, 5d, 5e, 5f, 5g, 5h, 5i, 6, 7 and 8), a variant of NOVX, at multiple of the mature form of NOVX. Also included are a polynuclectide encoding NOVX (or its complement), a vector comprising the polynuclectide, a cell comprising the vector, an anti-NOVX antibody, determining the presence of NOVX polynuclectide in a sample using the antibody of etermining the presence of NOVX polynuclectide in a sample using the process of NOVX polynuclectide in a sample using the nutibody. CC determining the presence of NOVX polynuclectide in a sample using a probe which binds to NOVX polynuclectide, in the polynuclectide and the antibody are useful for diagnosing, treating or preventing a NOVX.

CC antibody are useful for diagnosing, treating or preventing a NOVX. Cantibody are useful for diagnosing, treating or preventing a NOVX. Cantibody are useful for diagnosing, treating or preventing a NOVX. Cantibody are useful for diagnosing, treating or preventing a NOVX. Cantibody are useful for diagnosing, treating or preventing a NOVX. Cantibody are useful insignal processing and metabolic pathway modulation, inflammation, autoimmune disorders, selected from cardiomyopathy, attrose, Lesch-Nyhan graducerative and neuropsychiatric disorders, hypertension, wound has partingent disease, spreamic lapsace, Alzhaimer's disorders, hypertension, wound hearing, observe and neuropsychiatric disorders, hypertension, wound consumed the antibody are useful in screening assays, consumptioning clinical trials and pharmacogenomic), and in methods of treatment (e.g., chromosomal mapping, tissue tryping, forensic biology), consumed to modulate and antagonist compounds, and as bait proceductive medictine (e.g., diagnosetic assays) prognostic assays, conserved the presented of the presented of the presented of the produce antibodies immunospecific for NOVX, as vaccines to recent for potential agon membrane bound The invention relates to an isolated cytoplasmic, nuclear,

Sequence 415 AA;

Gaps ö 61.1%; Score 44; DB 5; Length 415; 62.5%; Pred. No. 3.5e+02; ive 2; Mismatches 1; Indels Query Match Best Local Similarity 62.5' ----- 5; Conservative

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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January 3, 2005, 15:45:27; Search time 46 Seconds (without alignments) 14.417 Million cell updates/sec

1 cgywltiwgc 10 Perfect score: Sequence: Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

478139 segs, 66318000 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Issued Patents AA:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		عد			SUMMARIES	
Result No.	Score	Query Match	Length DB	DB	ID	Description
-	44.5	61.8	1024	4	US-09-562-737-84	Sequence 84, Appl
8	43	59.7	492	4	US-09-107-532A-6945	694
٣	42.5	59.0	1024	4	US-09-562-737-86	
4	42.5	59.0	1765	4	US-09-354-147C-2	
S	42.5	59.0	1765	4	US-09-354-147C-3	٠,
9	42	58.3	161	4	US-09-325-932A-187	-
7	42	58.3	273	4	US-09-270-767-46926	7
80	42	58.3		4	US-09-792-616-9	
6	42	58.3		4	US-09-792-616-3	'n
10	41	56.9		4	US-09-071-035-408	408
11	41	56.9		4	US-09-134-000C-3630	3630
12	41	56.9	264	4	US-09-540-236-2978	
13	41	56.9		4	US-09-071-035-406	406, 7
14	40.5	56.2		4	US-09-562-737-81	Sequence 81, Appl
15	40.5	56.2		4	US-09-562-737-87	87,
16	40.5	56.2	1835	ო	US-08-836-325-15	Sequence 15, Appl
17	40.5	56.2		4	US-09-457-571-15	15,
18	40.5	56.2		4	US-10-162-012-24	24,
19	40.5	56.2	1969	٣	US-08-836-325-16	16,
20	40.5	56.2		4	US-09-457-571-16	16,
21	40.5	56.2		m	US-09-024-020B-9	o,
22	40.5	56.2	1976	ო	US-09-425-043-9	6
23	40.5	56.2	1977	4	US-09-976-594-757	75
24	40.5	56.2	1977	4	US-09-919-039-367	36
25	40.5	56.2	1978	m	US-09-024-020B-3	'n
56	40.5	56.2	1978	m	US-09-425-043-3	'n
27	40.5	56.2	1984	٣	US-08-836-325-10	Sequence 10, Appl

10, Appl	4, Appli	11, Appl	12, Appl	11, Appl	12, Appl	7, Appli	7, Appli	4, Appli	2, Appli	2, Appli	4, Appli	6, Appli	19350, A	4541, Ap	18, Appl	22, Appl
Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence
US-09-457-571-10 US-09-024-020B-4	US-09-425-043-4	US-08-836-325-11	US-08-836-325-12	US-09-457-571-11	US-09-457-571-12	US-08-836-325-7	US-09-457-571-7	US-09-634-920-4	US-09-514-907A-2	US-09-896-994-2	US-09-840-125-4	US-08-415-751-6	US-09-248-796A-19350	US-09-513-999C-4541	US-09-443-041A-18	US-09-443-041A-22
4 W	m	m	m	4	4	ო	4	m	4	4	4	,-	4	4	4	4
1984	1988	1989	1989	1989	1989	2005	2005	2016	2016	2016	2016	362	668	73	430	450
56.2	56.2	56.2	56.2	56.2	56.2	56.2	56.2	56.2	56.2	56.2	56.2	55.6	55.6	54.9	54.2	54.2
40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40	40	39.5	39	39
7 7 8 8	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Gaps
                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1024;
              Sequence 84, Application US/09562737
Fatent No. 6428967
GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Getthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSWO708 US/09/562,737
CURRENT APPLICATION NUMBER: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 84
LENGTH: 1024
                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-562-737-84
US-09-562-737-84
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1; 1; Indels Score 44.5; DB 4; Pred. No. 1.6e+02; 3; Mismatches 1; Query Match 61.8%; Best Local Similarity 54.5%; Matches 6; Conservative

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NESULT 2
US-09-107-532A-6945
US-09-107-532A-6945
Squares 6945, Application US/09107532A
Fatent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES AND THERAPEUTICS NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Magaachusetts
COUNTRY: USA ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC

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Sequence 2, Application US/09354147C Patent No. 6573067
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    754 CGEWIENMWGC 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CGYWL-TIWGC 10
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Pred. No. 3.1e+02;
1; Mismatches 2; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.7%; Score 43; DB 4; Length 492; 85.7%; Pred. No. 1.3e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 86, Application US/09562737

Sequence 86, Application US/09562737

GENERAL INFORMATION:
APPLICANT: Herz, Joachim
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT PILION UNWER: US/09/562,737
CURRENT PILION DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn Ver. 2.1
                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-507
INFORMATION FOR SEQ ID NO: 6945:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...492
SEQUENCE DESCRIPTION: SEQ ID NO: 6945:
US-09-107-532A-6945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Enterococcus faecium
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 492 amino acide
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.0%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 63.6
Matches 7; Conservative
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LENGTH: 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-562-737-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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RESULT 4

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| Sequence 2, Application US/0334147C |
| Regented 2, Application US/0334147C |
| Regented 3, Application US/0334147C |
| Regented 3, Application US/0334147C |
| Regented 4, Application Sequence 3, Application of Sedium Channels in Doreal Rock Ganglia |
| PILE REPRESSIVE 447-2004-01-US |
| CURRENT APPLICATION NUMBER: US/09/254,147C |
| PRIOR PRIOR COURTY NUMBER: PG |
| PRIOR PLING DATE: 1999-10-129 |
| PRI
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GENERAL INFORMATION:
APPLICANT: PXE International, Inc.
APPLICANT: EXE International, Inc.
APPLICANT: University of Hawaii
APPLICANT: University of Hawaii
ITILE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
TITLE OF INVENTION: Pseudoxanthoma Elasticum
FILE REFERENCE: PXE-0.01
CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT PILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 408, Application US/09071035
Patent No. 648043
PABENT NO. 648043
APPLICANT: G11 H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
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Pred. No. 5.2e+02;
2; Mismatches 0; Indels
                                                                          DB 4; Length 1498;
                                                                Score 42; DB 4; Deus-Pred. No. 5.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
APPLICATION DATA:

APPLICATION NUMBER: US/09/071,035
FILING DATE:
                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09792616
Patent No. 6780587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.3%;
                                                                       Query Match 58.3%;
Best Local Similarity 71.4%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 58.3
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
    ; ORGANISM: Mus musculus
US-09-792-616-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                          ||||::|
965 GYWLSLW 971
                                                                                                                                                                  2 GYWLTIW 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-09-071-035-408
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US-09-792-616-3
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                               Sequence 187, Application US/09325932A
Fatent No. 6451604
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Elasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant develor ILLE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT APPLICATION NUMBER: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 187
TYPE: PRT
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Patent No. 6780587

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PER International, Inc.
APPLICANT: PER International in a gene encoding an ABC transporter (MRP6) causing TITLE OF INVENTION: Pseudoxanthoma Blasticum
TITLE OF INVENTION: Pseudoxanthoma Blasticum
FILE REFERENCE: PXE-001
CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT PILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 9
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US-09-270-767-46926
US-09-270-767-46926
Sequence 46926, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster; FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DARF: 1999-03-17
NUMBER OF SEQ ID NOS: 62217
SOFTWARE: PatentIn Ver. 2.0
SEQ TO NO 46926
SERGIF - 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.3%; Score 42; DB 66.7%; Pred. No. 62; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Drosophila melanogaster US-09-270-767-46926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 GYWLNLSGC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GYWLTIWGC 10
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RESULT 6
US-09-325-932A-187
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US-09-792-616-9
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Sequence 406, Application US/09071035
Patent No. 6448043
GREEAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INFORTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TILLE OF INVENTION:
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT PILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 81
LENGTH: 1024
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                 ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/09/071,035
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Blookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8514
INFORMATION FOR SEQ ID NO: 406:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-562-737-81
; Sequence 81, Application US/09562737
; Patent No. 6428967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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                                          200 CGAWLGIW 207
    1 CGYWLTIW 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: six
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                        RESULT 13
US-09-071-035-406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-071-035-406
                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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Fatent No. 6673910
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 2709-2005-001
CURRENT APPLICATION ON WHERE: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2978
LENGTH: 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3630, Application US/09134000C

Sequence 3630, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: UNCEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTERCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BATER OCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT PILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR PILING DATE: 1997-08-15

SOFTWARE PERCENCE: PATENTIANG DATE: 1997-08-15

SEQ ID NO 3630

LENGTH: 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 4; Length 229;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                             Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                         Score 41; DB 4; 1
Pred. No. 1.2e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 408:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.9%;
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                        LENGTH: 222 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 62.5
Best Local Similarity 5.5
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-071-035-408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT

ORGANISM: M.catarrhalis

US-09-540-236-2978
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179 GTWITLWG 186
                                                                                                                                                                                                                                                                                                                                               2 GYWLTIWG 9
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US-09-540-236-2978
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ORGANISM: Artificial Sequence

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FEATURE:
JOTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-562-737-81
                                                                                                            Query Match 56.2%; Score 40.5; DB 4; Length 1024; Best Local Similarity 54.5%; Pred. No. 5.8e+02; Matches 5; Conservative 2; Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 56.2%; Score 40.5; DB 4; Length 1024; Best Local Similarity 54.5%; Pred. No. 5.8e+02; Matches 6; Conservative 2; Mismatches 2; Indels 1.
                                                                                                                                                                                                                                                                                                              RESULT 15
US-09-562-737-87
Sequence 87, Application US/09562737
Fatent No. 6428967
GENERAL INFORMATION:
APPLICANT: Herz, Joachim
TITLE OF INVENTION:
FILE REFRENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 87
LENGTH: 1024
                                                                                                                                                                                                                                || |: |:| |
892 CGEWIETMWDC 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CGYWL-TIWGC 10
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892 CGEWIGTMWDC 902
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Search completed: January 3, 2005, 15:53:49 Job time : 47 BECB

g

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

January 3, 2005, 15:52:22 ; Search time 142 Seconds (without alignments) 25.333 Million cell updates/sec Run on:

1 cgywltiwgc 10 Sequence:

SEQ33 72

Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1599051 seqs, 359727711 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 35, Appl	Sequence 34, Appl	Sequence 73, Appl	Sequence 2288, Ap	Sequence 1934, Ap	Sequence 476, App	Sequence 125253,	Sequence 54, Appl			Sequence 77862, A	Sequence 84, Appl	Sequence 181150,
	ΔI	US-10-046-922-35	US-10-046-922-34	US-10-046-922-73	US-10-017-161-2288	US-10-292-798-1934	US-10-280-066-476	US-10-437-963-125253	US-10-125-869A-54	US-10-462-262-278	US-10-112-944-743	US-10-282-122A-77862	US-10-211-962-84	US-10-437-963-181150
	90	13	13	13	14	14	14	16	14	15	15	15	14	16
	Query Match Length DB ID	10	10	10	304	304	25	63	17	17	136	828	1024	103
æ	Query Match	100.0	75.0	69.4	66.0	0.99	65.3	65.3	63.9	63.9	63.9	62.5	61.8	61.1
	Score	72	54	20	47.5	47.5	47	47	46	46	46	45	44.5	44
	Result No.	7	7	m	4	S	9	7	æ	σ	10	11	12	13

Sequence 54778, A Sequence 297, Appl Sequence 19313, Appl Sequence 19313, A Sequence 150191, Sequence 15314, Appl Sequence 1337, Appl Sequence 1337, Appl Sequence 1337, Appl Sequence 2, Appl Sequence 2, Appl Sequence 3, Appl Sequence 119, Appl Sequence 204612, Sequence 204612, Sequence 204612,
US-10-767-701-54778 US-10-125-869A-73 US-10-369-493-19313 US-10-369-493-19313 US-10-38-9493-19313 US-10-38-963-160191 US-10-38-963-160191 US-10-28-122A-57928 US-10-437-963-190740 US-10-364-237-245-1534 US-10-26-115-1337 US-10-296-115-1337 US-10-296-115-137 US-10-296-115-137 US-10-296-115-137 US-10-296-115-137 US-10-296-115-137 US-10-296-115-137 US-10-296-115-137 US-10-38-470-3 US-10-38-470-3 US-10-38-470-3 US-10-38-470-3 US-10-38-470-3 US-10-16-90-90 US-10-16-90 US-10-16-90 US-10-16-90 US-10-16-260-318 US-10-16-260-318 US-10-16-260-318 US-10-16-260-318 US-10-16-260-318 US-10-42-599-179308 US-10-425-115-312065
0 4 5 4 4 4 9 8 9 9 1 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
161 13 13 13 14 47 47 47 47 47 47 47 47 47 47 47 47 47
1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1
444444444 44 44 44 44 44 44 44 44 44 44
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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RESULT 1
US-10-046-922-35

$ Sequence 35, Application US/10046922

$ Sequence 35, Application US/10046922

$ Publication No. US20020164667A1

$ GENERAL INFORMATION:

$ APPLICANT: Alitalo, Kari

$ APPLICANT: Kubo, Hajime

$ TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS

$ TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS

$ CURRENT FILING DATE: 2002-01-15

$ NUMBER OF SEQ ID NOS: 80

$ SEQ ID NO 35

$ LENGTH: 10

LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: isolated peptide
US-10-046-922-35
```

100.0%; Score 72; DB 13; Length 10; 100.0%; Pred. No. 0.0026; Live 0; Mismatches 0; Indels RESULT 2
US-10-046-922-34
; Sequence 34, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki Query Match Best Local Similarity 100. Matches 10; Conservative 1 CGYWLTIWGC 10 1 CGYWLTIWGC 10 g ઠે

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Gaps

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APPLICANT: ABURATANI, HIROYUKI
TITLE OP INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
FRIOR APPLICATION NUMBER: US/10/246789
FRIOR PELLING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PARENTIN Ver. 2.1
LENGTH: 304
                                                                                                                                                                                                                                                                                                                                       LOCATION: (73)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEX: MOD RES
LOCATION: (19)..(83)
OTHER INFORMATION: Variable amino acid
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LOCATION: (897..(91)
OTHER INFORMATION: Variable amino acid
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OTHER INFORMATION: Variable amino acid
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LOCATION: (107)
OTHER INFORMATION: Variable amino acid
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JTHER INFORMATION: Variable amino acid
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OTHER INFORMATION: Variable amino
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OTHER INFORMATION: Variable amino
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OTHER INFORMATION: Variable amino
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                                                                                                                                                                                                                                                                                                               NAME/KEY: MOD_RES
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LOCATION: (85)
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LOCATION: (121)
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NAME/KEY: MOD RES
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NAME/KEY: MOD_RES
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NAME/KEY: MOD RES
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US-10-046-922-73
US-10-046-922-73

Sequence 73, Application US/10046922

Publication No. US20020164667A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Koivunen, Erkki
APPLICANT: Koivunen, Erkki
APPLICANT: Wow, Hajime
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 28667/37084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT PILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE PALENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.4%; Score 50; DB 13; Length 10; 60.0%; Pred. No. 2.5; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             75.0%; Score 54; DB 13; Length 10; 100.0%; Pred. No. 0.72; tive 0; Mismatches 0; Indels
    APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
FILLE REFERENCE: 2896/737084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 34
LENGTH: 10
                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: SITE
LOCATION:
OTHER INFORMATION: X is any amino acid
NAME/KEY: SITE
LOCATION: (10)...(10)
COTHER INFORMATION: X is any amino acid
COTHER INFORMATION: X is any amino acid
US-10-046-922-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE LOCATION: (9)..(9) OTHER INFORMATION: X is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (5)..(7)
OTHER INFORMATION: X is any amino acid
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Publication No. US20030143668A1
GENERAL INFORMATION:
APPLICANT: SUWA, MAXIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 60.0°
....hes 6; Conservative
                                                                                                                                                                                                         TYPE: PRT
ORGANISM: isolated peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
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LENGTH: 10
TYPE: PRT
ORGANISM: peptide library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||||||||
2 GYWLTIWG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GYWLTIWG 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-017-161-2288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Sequence 1934, Application US/10292798
; Sequence 1934, Application No. US200325833A1
; Publication No. US200325833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASUAL, MIXINA
; APPLICANT: ABUARANI, HIROYUKI
; TITLE OF INVENTION: GLANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR PILING DATE: 2001-12-18
; PRIOR PILING DATE: 2001-12-18
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEO ID NOS: 2070
; SOFTWARE: PatentIN Ver: 2.1
; SEQ ID NO 1934
                                                                                                                                                 ä
                                                                                                                                                 Gaps
                                                                                                     DB 14; Length 304;
                                                                                                                                               1; Indels
                                                                                                   ; Score 47.5; DB
; Pred. No. 88;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAME/KEY: MOD RES
COCATION: (80)..(83)
THER INFORMATION: Variable amino acid
; NAME/KEY: MOD_RES
; LOCATION: (256)..(289)
; OTHER INFORMATION: Variable amino acid
US-10-017-161-2288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MOD RES
LOCATION: (101)..(101)
OTHER INFORMATION: Variable amino acid
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LOCATION: (121)..(121)
OTHER INFORMATION: Variable amino acid
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INFORMATION: Variable amino acid
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OTHER INFORMATION: Variable amino acid
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LOCATION: (107)..(107)
JTHER INFORMATION: Variable amino acid
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THER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: MOD RES
LOCATION: (96)..(97)
OTHER INFORMATION: Variable amino
                                                                                                     66.0%;
                                                                                                   Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                 108 CGFW-AVWGC 116
                                                                                                                                                                                       1 CGYWLTIWGC 10
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NAME/KEY: MOD RES
LOCATION: (123)..(123)
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APPLICANT: Brissette, Renee
APPLICANT: Spruyt, Renee
APPLICANT: Spruyt, Michael
APPLICANT: Spruyt, Michael
APPLICANT: Dedova, Olga
APPLICANT: Brandergast, John
APPLICANT: Goldstein, Neil I.
TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BINDIFILE REPERENCE: 2598-4009US1
CURRENT APPLICATION NUMBER: US/10/280,066
FILE REPERENCE: 2002-10-24
RIOR APPLICATION NUMBER: 60/345,471
PRIOR APPLICATION NUMBER: 60/345,471
PRIOR APPLICATION NUMBER: 50/345,471
SEQ ID NOS: 537
SOFTWARE: PatentIn version 3.1
SEQ ID NO 476
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47.5; DB 14; Length 304; Pred. No. 88; 1; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.3%; Score 47; DB 14; Length 25; 66.7%; Pred. No. 13; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                FEATURE:

NAME/KEY: MOD RES;
COCATION: (219)..(219)
COTHER INFORMATION: Variable amino acid
FEATURE:
NAME/KEY: MOD RES
NAME/KEY: MOD RES
COTHER INFORMATION: (256)..(289)
COTHER INFORMATION: Variable amino acid
US-10-292-798-1934
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; Sequence 125253, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
                                            NAME/KEY: MOD RES
LOCATION: (178)...(178)
OTHER INFORMATION: Variable amino acid
                                                                                                              FEATURE:
NAME/KEX: MOD_RES
NAME/KEX: MOD_RES
OTHER INFORMATION: (211)
OTHER INFORMATION: Variable amino acid
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 476, Application US/10280066 Publication No. US20030180718A1 GENERAL INFORMATION: APPLICANT: Fillutla, Renuka C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MISC_FEATURE
OTHER INFORMATION: Tie1-20C-3-D116
                                                                                                                                                                                                                                                                                                                                                                                                                              66.0%;
60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 66.0
Best Local Similarity 60.0
Matches 6, Conservative
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Matches 6; Conservative
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15, ||| :||

5 CGYWGELWG 13
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US-10-280-066-476
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NAME/KEY: misc feature
LOCATION: (1)...(136)
OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: immunoglobulin binding polypeptide US-10-462-262-278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 63.9%; Score 46; DB Similarity 66.7%; Pred. No. 13; 6; Conservative 1; Mismatches
                                                                                                                        FILE REFERENCE: 10280-052001
CURRENT APPLICATION NUMBER: US/10/462,262
CURRENT FILING DATE: 2003-06-16
FRIOR APPLICATION NUMBER: US 60/388,642
FRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 430
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 278
LENGTH: 17
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PRIOR FILLING DATE: 2000-01-25
PRIOR PELICATION NUMBER: US 09/491,404
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR PELING DATE: 2000-02-03
PRIOR PELING DATE: 2000-02-28
PRIOR PELING DATE: 2000-03-07
PRIOR PILLING DATE: 2000-03-07
PRIOR PILLING DATE: 2000-03-07
PRIOR PILLING DATE: 2000-03-11
PRIOR PILLING DATE: 2000-03-11
PRIOR PILLING DATE: 2000-03-11
PRIOR PILLING DATE: 2000-03-18
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Sequence 743, Application US/10112944
Publication No. US20040048249A1
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tang, Y. Tom
APPLICANT: Yang, Yonghong
APPLICANT: Weng, Gezhi
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Nen, Feiyan
APPLICANT: Weng, Jian-Rui
APPLICANT: Wenrman, Tom
APPLICANT: Wenrman, Tom
APPLICANT: Weng, Dunrui
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Rang, Zhiwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 CGFWPRIWG 12
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Best Local Similarity
Matches 6; Conserv
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APPLICANT: Wu, Wei

APPLICANT: Wu, Wei

APPLICANT: Buckharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(5321)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 125253

LENOTH: 63

TYPE:
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Pred. No. 28;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Wu, Qi-Long
APPLICANT: Wu, Qi-Long
APPLICANT: Ley, Arthur C.
APPLICANT: Stochl, Mark
APPLICANT: Stochl, Mark
APPLICANT: Ransohoff, Thomas C.
APPLICANT: Potter, M. Daniel (deceased)
TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 3421.1006-001
CURRENT APPLICATION NUMBER: US/10/125,869A
CURRENT FILING DATE: 2002-11-19
FRIOR APPLICATION NUMBER: 60/284,534
PRIOR APPLICATION NUMBER: 60/284,534
NUMBER OF SEQ ID NOS: 200
NUMBER OF SEQ ID NOS: 200
SOFTWARE: FRAEKEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_27915C.1.pep
US-10-437-963-125253
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; Sequence 54, Application US/10125869A
; Publication No. US20030199671A1
; GENERAL INFORMATION:
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; Publication No. US20040009534A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 65.3%;
Best Local Similarity 60.0%;
Matches 6; Conservative
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 CGHYLKAWGC 46
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4 CGFWPRIWG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CGYWLTIWG 9
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LENGTH: 17
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US-10-437-963-181150
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR PLING DATE: 2000-05-06

PRIOR PLING DATE: 2000-05-06

PRIOR PLING DATE: 2000-05-06

PRIOR PLING DATE: 2000-05-06

PRIOR PLING DATE: 2000-05-07

PRIOR PLING DATE: 2000-05-07

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-110-23

PRIOR PLING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PLING DATE: 2001-12-22

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Xu, H. Tidentification of Essential Genes in Microorganisms
                                                                                                                                                 Gaps
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                                                                                Score 46; DB 15; Length 136;
Pred. No. 73;
1; Mismatches 3; Indels
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Pred. No. 4.3e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 77862, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
OTHER INFORMATION: in Example 2
                                                                                63.9%;
60.0%;
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SEQ ID NO 77862
LENGTH: 828
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Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                          Query Match
Best Local Similarity 60.0°
"--rhas 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 CGLWLELLSWGC 383
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US-10-282-122A-77862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGYWLTI--WGC 10
                                                                                                                                                                                                                                           93 CGRWDWLWGC 102
                                                                                                                                                                                                      1 CGYWLTIWGC 10
                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-10-282-122A-77862
                     US-10-112-944-743
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RESULT 12 US-10-211-962-84

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Sequence 181150, Application US/10437963

Sequence 181150, Application US/10437963

Sequence 181150, Application VG US2040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Shou, Yihua

APPLICANT: Shou, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 181150

LENGTH: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Sequence 84, Application US/10211962

Publication No. US20030082640A1

GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Gotthard, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/10/211,962
CURRENT FILING DATE: 2002-08-01
FRIOR APPLICATION NUMBER: US/09/562,737
PRIOR FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 84

IENGTH: 1024
TYPE: PRT
CRAINING ALLificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT4530_78451C.1.pep
US-10-437-963-181150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.8%; Score 44.5; DB 14; 54.5%; Pred. No. 6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h Similarity 50.0%; Pred. No. 1.1e+02; 4; Conservative 4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-10-767-701-54778
Sequence 54779, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||:|: |:| |
892 CGHWIETMWDC 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CGYWL-TIWGC 10
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ORGANISM: Oryza Bativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y ... Y 3 YWLTIWGC 10
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Matches 4; Conserv
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535) B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 54778
LENGTH: 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                            Query Match 61.1%; Score 44; DB 16; Length 161; Best Local Similarity 75.0%; Pred. No. 1.6e+02; Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.7%; Score 43; DB 14; Length 13; 62.5%; Pred. No. 27; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-10-125-869A-73
Sequence 73, Application US/10125869A
Publication No. US20030199671A1
GENERAL INFORMATION:
APPLICANT: Rondon, Isaac Jesus
APPLICANT: Ruthur C.
APPLICANT: Ety, Arthur C.
APPLICANT: Stochl, Mark
APPLICANT: Potter, M. Daniel (deceased)
ITLE OF INVENTION: POLYEPTIDES
FILE REFERENCE: 3421.1006-001
CURRENT FILING DATE: 2001-04-18
PRIOR PRILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-04-18
NUMBER OF SEC ID NOS: 200
SOFTWARE: PSEC FOR Windows Version 4.0
SEC ID NO 73
LENGTH: 13
TYPE: PRI
CURRENT: Attificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Pc region binding polypeptide
                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: 14593586.pep
US-10-767-701-54778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 CGYWLKPW 157
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                                                                                                                                                                                                                                                                                            FEATURE:
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Search completed: January 3, 2005, 16:04:48 Job time : 153 Becs

2 GYWLTIWG 9 | | | : | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | | 1 | |

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                  Copyright
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 protein search, using sw model OM protein

Run on:

January 3, 2005, 15:41:46; Search time 38 Seconds (without alignments) 25.320 Million cell updates/sec

1 cgywltiwgc 10 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	hypothetical prote	بد	_	channel	proteir	probable transport	multidrug resistan	oxaloacetate decar	hypothetical prote		permease [imported	hypothetical prote	sodium channel alp	channel		channel	channel	channel	sodium channel alp		channel	channel	channel		-	sodium channel alp	channel	sodium channel pro	sodium channel pro
В	S76385		T30902	T42388	230980	C95307	-	F70439	T48166	PC4117	E90446	T29407	I48108	A55138	A45380	CHEE	154323	I64893	JS0648	151964	CHRTM1	800320	I56555	S54771	A60054	A46269	B25019	A25019	A38195
08	2	~	~	~	~	~	N	7	~	~	N	7	7	~	~	-	~	~	N	~	-	~	~	~	~	~	~	~	~
Length	218	828	1993	1765	72	441	1502	620	307	391	419	739	200	1681	1682	1820	1835	1836	1836	1836	1840	1951	1976	97	1983	8	2005	8	5
& Query Match	63.9	62.5																		56.2									
Score	46	45	43.5	•	42	42	₹*	41.5	41	41	41	41	。	ö	ö	ö	ö	ö	٥.	40.5	ö	ö		ö	٠	•	ö	•	Ö
Bult No.		۲3	m	4	'n	ø	7	ω	თ	2	11	12	13	14	15	16	17	18	19	20	21	22	53	24	22	56	27	78	59

godium channel pro	sodium channel pro	Ig heavy chain pre	phenylalanyl-tRNA	probable ABC trans	probable Na+/H+-ex	probable ABC trans	genome polyprotein	probable aldo/keto	D-amino-acid oxida	D-amino-acid oxida	D-amino-acid oxida	D-amino-acid oxida	hypothetical prote	neurexin III beta	neurexin III beta
A33996	T43161	C34903	F97190	F95406	B71038	C95282	S64740	AH0289	JH0185	OXPGDA	501340	JX0132	AF1978	A53580	B53580
~	0	7	~	~	~	~	~	~	-	-1	-	-	C\$	~	N
2019	2049	142	339	359	425	508	2344	298	345	347	347	347	376	392	426
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26	29	55	55	5	55	55	5	54	54.9	54	54	54	54	54	54
40.5	40.5	40	40	40	40	40	40	39.5	39.5	39.5	39.5	39.5	39	39	39
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Gispecies: Synechocystis sp.
Ajvariety: PCC 6803
Cjbacies: Synechocystis sp.
Cjbacies: Spr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
Cjbacession: S76385
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis A,Accession: S76385
A,Status: preliminary
A,Rolecule type: DNA
A,Rolecule type: DNA
A,Residues: 1-218 <KAN>
A,Residues: 1-218 <KAN>
A,Rosserreferences: UNIPROT:Q55705, EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAA10237
A,Cross-references: UNIPROT:Q55705, EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAA10237
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: probable alkaline phosphatase yngC ö Gaps ö Length 218; 2; Indels hypothetical protein - Synechocystis sp. (strain PCC 6803) A; Reference number: S74322; MUID: 97061201; PMID: 8905231 DB 2; Score 46; DB; Pred. No. 8.1; 1; Mismatches Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative 73 CGYWVGRWG 81 1 CGYWLTIWG 9 876385 ò ద

RESULT 2

AD0412 ATP-dependent helicase [imported] - Yersinia pestis (strain CO92)

Gracession: AD0412
R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B., deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; if il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, R. Nature 413, 523-527, 2001
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; A; Cession: AD0412
A; A; Cession: AD0412
A; Status: preliminary
A; Molecule rype: DNA
A; Residues: 1-828 «KUR>
A; Residues: 1-828 «KUR>
A; Rossereferences: UNIPROT: Q8ZBL4; GB: ALS90842; PIDN: CAC92624.1; PID: g15981320; GSPDB: G; Genetics:

C;Genetics: A;Gene: hrpB C;Superfamily: ATP-dependent RNA helicase, HrpB type

62.5%; Score 45; DB 2; Length 828; Query Match ö

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probable transport protein SMa0684 [imported] - Sinorhizobium meliloti (strain 1021) mage C; Species: Sinorhizobium meliloti
C; Species: Sinorhizobium meliloti
C; Species: Sinorhizobium meliloti
C; Species: 24-Aug-2001 #text_change 09-Jul-2004
R; Stanset: M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Veh, K.C., Prock, M.C.; Surzycki, R.; Wells, D.H.; Veh, K.C., A; Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilots A; Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-41 - KUR>
A;Residues: 1-41 - KUR>
A;Cross-references: UNIPROT:092ZTG; GB:AB006469; PIDN:AAK65021.1; PID:g14523451; GSPDB:GP
A;Cross-references: UNIPROT:092ZTG; GB:AB006469; PIDN:AAK65021.1; PID:g14523451; GSPDB:GP
A;Cross-references: UNIPROT:092ZTG; GB:AB006469; PIDN:AAbola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Coi. Hyman, R.W.; Jones, T.
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.(A;Tele: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; WUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: T42216
R;Hirohashi, T.; Suzuki, H.; ILO, K.; Ogawa, K.; Kume, K.; Shimizu, T.; Sugiyama, Y.
Mol. Pharmacol. 53, 1068-1075, 1998
A;Title: Hepatic expression of multidrug resistance-associated protein-like proteins mair
A;Reference number: Z22081; MUID:98279126; PMID:9614210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-1502 <HIR>
A;Cross-references: UNIPROT:088269; EMBL:AB010466; NID:g3242457; PIDN:BAA28954.1; PID:g3;
A;Experimental source: strain Sprague-Dawley; liver
                                                                                     EMBL:Z18946; NID:g15859; PIDN:CAA79411.1; PID:g15891 submitted to the EMBL Data Library, December 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 441;
                                                                                                                                                                                                                               Length 72
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                            Score 42; DB 2
Pred. No. 12;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 3
Pred. No. 58;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Genome: plasmid
C;Superfamily: L-lysine transport protein
                                A;Molecule type: DNA
A;Residues: 1-72 <DON>
A;Cross-references: UNIPROT:Q05245;
A;Note: the nucleotide sequence was C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.3%;
71.4%;
                                                                                                                                                                                                                               58.3%;
62.5%;
                                                                                                                                                                                                                                                                                       5; Conservative
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GYWISIW 98
                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                   50 CGMWLPVW
                                                                                                                                                                                                                                                                                                                                              1 CGYWLTIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
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310980
gene 315 protein - Mycobacterium phage L5
G'Species: Mycobacterium phage L5
C'Species: Mycobacterium 30-Sep-1993 #text_change 09-Jul-2004
R'Sponnelly-Wu, M.K.; Jacoba Jr., W.R.; Hatfull, G.F.
Mol. Microbiol. 7, 407-417, 1993
MyTitles: Superinfection immunity of mycobacteriophage L5: applications for genetic trans A;Reference number: $30949; MUID:93211283; PMID:8459767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Experimental source: strain Sprague-Dawley; dorsal root ganglia
A;Note: preferentially expressed in sensory neurons within dorsal root ganglia and trige
C;Superfamily: sodium channel protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-1765 <DIB>
A;Cross-references: UNIPROT:O88457; EMBL:AP059030; NID:g3372614; PID:g3372615; PIDN:AAC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPROT:P90670; EMBL:U66915; NID:g1842248; PID:g1842249; PIDN:AAC474
C,Superfamily: sodium channel protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA.
                                                                                                                                                                                                                                                                                 sodium channel SCAP1 alpha chain - California sea hare
C;Species: Aplysia californica (California sea hare)
C;Decies: Aplysia californica (California sea hare)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30902
R;Dyer, J.R.; Johnston, W.L.; Castellucci, V.F.; Dunn, R.J.
A;Tile: Ohnston, W.L.; Castellucci, V.F.; Dunn, R.J.
A;Tile: Cloning and tissue distribution of the Aplysia Na+ channel alpha-subunit
A;Reference number: Z20329; MUD:97238630; PMID:9115644
                                   ;
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                   5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.0%; Score 42.5; DB 2; Length 1765; 54.5%; Pred. No. 1.6e+02; ive 2; Mismatches 2; Indels 1
                                   Indels
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A;Molecule type: mRNA
        Pred. No. 36;
1; Mismatches
  58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 54.5%;
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sodium channel alpha chain - rat
                                                                                                                                               372 CGLWLELLSWGC 383
     Best Local Similarity 58.3
Matches 7; Conservative
                                                                                        1 CGYWLTI--WGC 10
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permease [imported] - Sulfolobus solfataricus
permease Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: E90446
R;Sho, Q; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-volong, I.; Joffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, Parmitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: E90446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:097VB7; GB:AE006641; NID:g13816037; PIDN:AAK42828.1; GSPDB:GP
C;Genetics:
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A.Map position: 2
A.Introns: 68/2; 179/3; 253/1; 275/3; 327/2; 365/3; 397/1; 428/2; 463/3; 629/1; 668/2; 7;
                          replication protein homolog - Pyrococcus sp. (fragment)
NyAlternate names: hypothetical 391 protein
C;Specias: Pyrococcus sp.
C;Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 17-May-1996
C;Accession: PC4117
R;Rashid, N.; Morikawa, M.; Imanaka, T.
Gene 166, 139-143, 1995
A;Title: An abnormally acidic TATA-binding protein from a hyperthermophilic archaeon.
A;Reference number: JC4514; MJD:96105215; PMID:8529878
A;Accession: PC4117
A;Molecule type: DNA
A;Residues: 1-391 «RAS>
A;Cross-references: DDBJ:D50018
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T29407
R;Waterston, R.; Le, T.T.; Gattung, S.
R;Reference number: 220617
A;Reference number: 220617
A;Re
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74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB :
Pred. No. 74;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 56.9%;
Best Local Similarity 85.7%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 YWLTEWG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GYWLTIWG 9
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Best Local Similarity
Matches 5; Conserv
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A;Molecule type: DNA
A;Residues: 1-419 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/biot
F;S40-613/Domain: lipoyl/biotin-binding homology <LPB>
F;S79/Binding site: biotin (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
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C; Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: P70439
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein T1008.150 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48166
R;Bevan, M ; Pohl, T ; Weizenegger, T ; Bancroft, I ; Mewes, H.W ; Lemcke, K ; Mayer, alterance number: 224486
A;Accession: T48166
A;Accession: T48166
A;Steurus preliminary
A;Molecule type: DNA
A;Residues: 1-307 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: F70439
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                                                                        Length 1502;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   decarboxylase alpha chain - Aquifex aeolicus
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A;Experimental source: cultivar Columbia; BAC clone T1008
                                                                        58.3%; Score 42; DB 2; I ilarity 71.4%; Pred. No. 1.7e+02; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 5
A;Introns: 31/3; 66/2; 114/3; 149/2; 232/2; 284/1
A;Note: T1008.150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.6%; Score 41.5; D
60.0%; Pred. No. 93;
iive 2; Mismatches
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Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 50.0
Matches 5, Conservative
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                                                                                                                                                                                                                                                                    964 GYWLSLW 970
                                                                    Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                      2 GYWLTIW 8
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686 CGEWVETLWDC 696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Godium channel alpha subunit - long-tailed hamster (fragment)
C:Species: Cricetulus longicaudatus (long-tailed hamster)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: 148108
R:Lalik, P.H.; Krafte, D.S.; Ciccarelli, R.B.
Am. J. Physiol. 264, 803-809, 1993
A:Title: Characterization of endogenous Sodium channel gene expressed in chinese hamster
A:Reference number: 148108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-200 <RES>
A;Cross-references: UNIPROT:Q60464; GB:M87541; NID:g191069; PIDN:AAA36979.1; PID:g553840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Godium channel mNa2.3, voltage-gated - mouse ("Species: Mus musculus (house mouse) ("Species: Mus musculus (house mouse) ("Species: No. Musculus (house mouse) ("Species: No. Musculus (house mouse) ("Species: No. Musculus (house mouse) ("State: No. Musculus (house mouse) ("State: No. Musculus ("State: Musculus
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A;Cross-references: UNIPROT:Q62467; GB:L36179; NID:g609544; PIDN:AAA66192.1; PID:g806397
C;Superfamily: sodium channel protein
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C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A45380
R;George Jr., A.L.; Knittle, T.J.; Tamkun, M.M.
                                                                                                                                                                                 Gaps
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Pred. No. 49;
                                                                        Query Match 56.9%; Score 41; DB 2; Length 739; Best Local Similarity 60.0%; Pred. No. 1.38+02; Matches 6; Conservative 1; Mismatches 3; Indels
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C;Superfamily: myeloperoxidase; myeloperoxidase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
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C,Superfamily: sodium channel protein
C,Keywords: duplication
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Matches 6; Conservative
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118 CGFWATIREC 127
                                                                                                                                                                                                                                                               1 CGYWLTIWGC 10
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Proc. Natl. Acad. Sci. U.S.A. 89, 4893-4897, 1992

A; Title: Molecular cloning of an atypical voltage-gated sodium channel expressed in human A; Reference number: A45380; MUID:92279233; PMID:1317577
A; Rocession: A45380
A; Status: nucleic acid sequence not shown A; Nolecule: Type: mRNA A; Residues: 1-1682 acid sequence not shown A; Residues: 1-1682 acid sequence over sequence source: heart A; Residues: 1-1682 acid source: heart A; Residues: 1-1682 acid source: heart C; Reywords: glycoprotein; membrane protein; phosphoprotein; sodium channel protein C; Superfamily: sodium channel protein C; Reywords: glycoprotein; membrane protein; phosphoprotein; sodium channel; voltage-gatec Query Match S6.2%; Score 40.5; DB 2; Length 1682; Best Local Similarity 54.5%; Pred: No. 3.1e+02; Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 CGYWL-TIWGC 10
| | | | | | | | | | | D | C68 CGEWVETLWDC 696
Search completed: January 3, 2005, 15:52:58
Job time: 39 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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	January 3, 2005, 15:30:50 ; Search time 188 Seconds
	Sea
OM protein - protein search, using sw model	2005, 15:30:50 ;
rch,	3,
protein sea	January
- -	
OM prote	Run on:

(without alignments)
30.605 Million cell updates/sec

Title:
SEQ33
Perfect score: 72
Sequence: 1 cgywltiwgc 10
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1	Description	Q55705 synechocyst		Q8dla7 yersinia pe	66 yersini	P90670 aplysia cal		Q74jk6 lactobacill	Aas08923 lactobaci	Q6c574 yarrowia li	Q8dkd6 synechococc		Q7wy20 pseudomonas		homo	Q9nrw9 homo sapien	Q96pl4 homo sapien	Aar25556 homo sapi	Q7yyfl cryptospori		Q05245 mycobacteri	Q85513 mycobacteri	Q6mc01 parachlamyd	9	Q94f82 cajanus caj		Q92zt6 rhizobium m	Q83g14 tropheryma	_	9	Q9xd77 nitrobacter	Q8vq84 nitrosospir
	TT.	Y232_SYNY3	Q8ZBL4	Q8D1A7	AAS60566	P90670	Ф6Н022	Q74JK6	AAS08923	Q6C574	QBDKD6	Q8H2N7	Q7WY20	Q96AC0	Q6RW13	Q9NRW9	Q96PL4	AAR25556	Q7YYF1	088457	VG35_BPML5	Q855 <u>1</u> 3	Q6MC01	CAF23898	Q94FS2	083151	Q92ZT6	Q83G14	RBL_NITVU	Q9X <u>D</u> 76	Q9XD77	Q8VQ84
8	3 :	Н	N	~	~	0	~	~	~	N	~	~	~	~	~	~	0	~	~	~	Н	~	~	~	N	~	~	~	⊣.	~	~	8
1	rengen	218	828	853	853	1993	168	221	221	501	646	733	1084	152	159	159	159	159	263	1765	72	133	284	₿	343	389	441	452	472	473	473	473
Query	MACCI	63.9		62.5	62.5	60.4			59.7	59.7	59.7	59.7	59.7	59.0	59.0	29.0	59.0	59.0	59.0	59.0	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3
9	Score	46	45	45	45	43.5	43	43	43	43	43	43	43	42.5	42.5	42.5	42.5	42.5	42.5	42.5	42	42	42	42	42	42	42	42	42	42	42	42
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Q8t6h2 dictyosteli	-	O88269 rattus norv	O95255 homo sapien	Q8n1z5 homo sapien	067544 aquifex aeo	Q82z85 enterococcu	Q9m030 arabidopsis		Q8iud8 homo sapien		Q97vb7 sulfolobus	Q6nur0 homo sapien	Aah59368 homo sapi
Q8Т6H2	MRP6 MOUSE	MRP6_RAT	MRP6_HUMAN	Q8N1 <u>Z</u> 5	067544	082285	Q9M030	Q6CBE4	Q8IUD8	ОЭНКАЭ	Q97VB7	Q6NUR0	AAH59368
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42 58.3	42 58.3	42 58.	42 58		41.5 5		41 5	41	41	41	41	41	41

ALIGNMENTS

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Bacteriol. 184:4601-4611(2002)
                                        SEQUENCE FROM N.A.
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STRAIN=KIMS, / Biovar Mediaevalis;
MEDLINE=22137863; pubmed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R., "Genome sequence of Yersinia pestis KIM.";
                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN=CO-92 / Biovar Orientalis;

STRAIN=CO-92 / Biovar Orientalis;

BabLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,

"Genome sequence of Yersinia pestis, the causative agent of plague.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Enterobacteriaceae; Yersinia.
NCBI_TaxID=632;
                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
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01-MAR-2003 (TFEMBLrel. 23, Created)
01-MAR-2003 (TFEMBLrel. 23, Last sequence update)
01-OCT-2004 (TFEMBLrel. 28, Last annotation update)
Halicase, ATP-dependent.
Name-hrpB: OrderedLocusNames=YP0291, y0794;
Versinia pestis
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         853 AA.
                   ATP-dependent helicase.
Name=hrpB; OrderedLocusNames=YPO3394;
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                                                                                                                                                                                                                                                                                                                                                                                          Nature 413:523-527(2001).
EMBL; AJ414156; CAC92624.1; -.
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                                                               Yersinia pestis.
                                                                                                                       NCBI_TaxID=632;
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STRAIN-91001 / Biovar Mediaevalis;
SONG Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
SONG Y., Tong X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
Yang R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
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                                   Zhou
STRAIN=91001 / Biovar Mediaevalis;
Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zho
Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.
Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
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                                                                                                               Yang R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AE013681; AAM84381.1;
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000826; F:ATP-dependent helicase activity; IEA.
GO; GO:0004886; F:Phelicase activity; IEA.
GO; GO:0004887; F:helicase activity; IEA.
GO; GO:0005687; F:helicase activity; IEA.
GO; GO:0005687; F:helicase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TICRFAMB; TICR01970; DEAH box HrpB; 1.
ATP-binding; Helicase; Hydrolase.
SEQUENCE 853 AA; 95004 MW; B3DB738A18665B42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 853 AA; 95004 MW; B3DB738A18665B42 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR011410; DEAD.
InterPro; IPR011545; DEAD/DEAH N.
InterPro; IPR011545; DEAH/DOX-HrpB.
InterPro; IPR01150; Helicase_dom.
Pfam; PF00270; DEAD; 1.
Pfam; PF00470; DEAD; 1.
Pfam; PF00470; HA2; 1.
Pfam; PF00470; Helicase_dom.
Pfam; PF00470; Helicase_dom.
Pfam; PF00470; Helicase_dim.
SWART; SW00487; DEXDC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397 CGLWLELLSWGC 408
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221 AA
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    J. Bacteriol. 186:4338-4349(2004).

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05-JUL-2004 (TrEMBLrel. 27, C.
05-JUL-2004 (TrEMBLrel. 27, L.
05-JUL-2004 (TrEMBLrel. 27, L.
Hemolyain-like procein.
OrderedLocueNames=LJ1101;
                                                                                                                                                                       59.7%;
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02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 07-MAR-2004 (TrEMBLrel. 27, 07-4004)
                                                                                                                                                                         Query Match 59.7
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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172 GFWLLVWG 179
                                                                                                                                                                                                                                           1 CGYWLTIWG 9
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                                 SEQUENCE FROM N.A.
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PubMed=14966310;
                                                   STRAIN=FD33;
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Q74JK6
ID Q74J
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AAS08923
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                                                   01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
Sodium channel alpha-subunit SCAPI.
Aplysia californica (California sea hare).
Bukaryota: Mecazoa, Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
NCBI_TaxID=6500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                 DNA Cell Biol. 16:347-356(1997).
-!- SUBCELLUIAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to the sodium channel family.
-- BIBL, U66915; AAG47457.1; -.
PIR; T30902; T30902.
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUB-Nervous system;
MEDLINE-97238630; PubMed=9115644;
Dyer 'J.R., Johnston W.L., Castellucci V.F., Dunn R.J.;
"Cloning and tissue distribution of the Aplysia Na+ channel alphasubunit cDNA";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GG; GG: 0016621; C: integral to membrane; IEA.

GG; GG: 001651; C: integral to membrane; IEA.

GG; GG: 0001518; C: voltage-gated sodium channel complex; IEA.

GG; GG: 0005261; F: cation channel activity; IEA.

GG; GG: 0006812; F: cation transport; IEA.

R GG; GG: 0006812; P: cation transport; IEA.

R InterPro; IPR001682; Ca/Na pore.

R InterPro; IPR001582; Ion trans.

R InterPro; IPR005821; Ion trans.

R InterPro; IPR005821; Ion trans.

R InterPro; IPR005820; Na channel nig.

R InterPro; IPR001696; Na channel nig.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Fremyella diplosiphon (Calothrix PCC 7601).
Bacteria: Cyanobacteria; Nostocales; Microchaetaceae; Fremyella.
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STRAIN=FD33;
Stowner Evans E.L., Ford J., Kehoe D.M.;
Genomic DNA Microarray Analysis: Identification of New Genes
Regulated by Light Color in the Cyanobacterium Fremyella
diplosiphon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 60.4%; Score 43.5; DB 2; Length 1993; Best Local Similarity 54.5%; Pred. No. 8.9e+02; Matches 6; Conservative 3; Mismatches 1; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00520; Ion_trans; 4.—
Pfam; PF06512; Na_trans assoc; 1.
PRINTS; PR00170; NACHANNEL.
Ion transport; Ionic channel; Sodium channel; Transmembrane; Transport; Voltage-gated channel.
SEQUENCE 1993 AA; 225896 MW; 33E174B9BF07E1A7 CRC64;
                                                 PRT; 1993 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 AA
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                                                 PRELIMINARY;
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              RESULT 5
P90670
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064022
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InterPro: IPR004254; HJyIII related.
InterPro: IPR005744; HJyIII related.
InterPro: IPR005744; HJyIII related.
ITGRPAMS; TIGR01065; HJyIII; 1.
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                                                                                                                                                                                                                      1; Indels
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
NCBI_TaxID=33959;
Stowner Evans E., Ford J., Kehoe D.M.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databages.
EMBL, AY548455; AAT41947.1; -.
Hypothetical protein.
SEQUENCE 168 AA, 18932 MW; 1C9DB963D5210332 CRC64;
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Last annotation update)
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Last annotation update)
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Pred, No. 1.1e+02;
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646 AA

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MEDLINE=2225144; PubMed=12240834;
Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein OJ1138_B05.118.
Name=OJ1138_B05.118;
Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 59.7%; Score 43; DB 2; Length 646; Best Local Similarity 62.5%; Pred. No. 3.7e+02; Matches 5; Conservative 1; Mismatches 2; Indels
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                                                                                                                                                                      OrderedLocusNames=t110923;
Synechococcus elongatus (Thermosynechococcus elongatus)
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 646 AA; 71071 MW; 56C5A74F76652D56 CRC64;
                         QBDKD6;
01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Tl10923 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 9:123-130(2002).

EMBL, AP005372; BAC08475.1; -.

CO, GO:0003824; F:catalytic activity; IEA.

InterPro; IPR001932; PP2C-like.

Pfam; PF00481; PP2C; 1
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PRT;
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SMART; SM00331; PP2C_SIG; 1.
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Gramene; Q8H2N7; -.
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Best Local Similarity 85.73
Matches 6; Conservative
PRELIMINARY;
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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Goffard N., Frangeul L., Aigle M., Anthourd V., Babour A., Barbe V.,
Goffard N., Frangeul L., Aigle M., Anthourd V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykaeten C.,
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Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
M., Genome evolution in yeasts.",
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                 Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C., Pridmore R.D., Zwahlen M.-C., Rouvet M., Altermann B., Barrangou R., Morcenier A., Klaenhammer T., Arigoni F., Schell M.A.; Lactobacillus johnsonii NCC 533."; Processillus johnsonii NCC 533."; Processillus johnsonii NCC 533."; Processillus johnsonii NCC 533."; Processillus Jakon Jako
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-071-2004 (TrEMBLrel. 28, Created)
01-071-2004 (TrEMBLrel. 28, Last sequence update)
01-071-2004 (TrEMBLrel. 28, Last sequence update)
01-071-2004 (TrEMBLrel. 28, Last annotation update)
Chromosome E of strain (LIB99 of Yarrowia lipolytica.
ORFNames=YALIOE20471g;
Sarrowia lipolytica (Candida lipolytica).
Bukaryota; Pungi; Sacomycota; Saccharomyceties;
Saccharomycetales; Dipodascaceae; Yarrowia.
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                                                                                                                                                                                                                                                                                                                                                              Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382131; CAG79783.1; -.
SEQUENCE 501 AA; 56411 MW; 91F08EF5A63C60FB CRC64;
                                                                                                                                                                                                                                                                                                                                                              59.7%; Score 43; DB 2; I 62.5%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 62.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||:||:|
GYYLTLWYC 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 GFWLLVWG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GYWLTIWG 9
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4952;
                                  STRAIN=NCC 533;
PubMed=14966310;
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GENOLEVURES;
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RESULT 9

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Gaps

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733 AA.

ö ö 59.7%; Score 43; DB 2; Length 733; 85.7%; Pred. No. 4.2e+02; cive 0; Mismatches 1; Indels InterPro; IPR007658; DUF594. Pfam, PF04578; DUF594; 1. Hypothetical protein. SEQUENCE 733 AA; 82939 MW; E95884DADIDC2AC9 CRC64;

RESULT 10 Q8DKD6

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07WY20

RESULT 12

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MEDLINE=22388257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Itachul S.F., Zeeberg B., Wagner L., Sheamen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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Krzywinski M.I., Skalsku U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O., Rajkumar N., Yi O., Nickerson D.A.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY488088; AAR25556.1; -...
EGO, GO.004872; F:receptor activity; IEA.
InterPro; IPR009436; AGTRAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.0%; Score 42.5; DB 2; Length 152; 70.0%; Pred. No. 1.2e+02; ive 1; Mismatches 1; Indels :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017328; AAH17328.1; -.
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SEQUENCE 152 AA; 16669 MW; 637C01214175C3C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 AA; 17419 MW; 7E1D5C7E79AE6BC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro; IPR009436; AGTRAP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GYW-LTIWGC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 GHWLLTTWGC 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. TISSUE=Colon;
                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
NCBI_TaxID=9606;
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QGRW13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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READER SERVICE SERV
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"In Smill ARITY: Contains 1 histidine kinase domain.

"EMBL. AV273869; AAP84165.1; -..

"BEMBL. AV273869; AAP84165.1; -..

"BEMBL. AV273869; AAP84165.1; -..

"BEMBL. AV273869; AAP84165.1; -..

"BEMBL. AV273867; F.NAT Dinding; IEA.

"GO; GO:0005524; F.ATP Dinding; IEA.

"GO; GO:000156; F:kno-component sensor molecule activity; IEA.

"GO; GO:000156; F:two-component signal transduction system (p. ..; IEA.)

"BEMBL. AV273867; His kinase.

"InterPro; IPR003594; ATP810A ATP828e.

"InterPro; IPR003507; His kinase.

"InterPro; IPR003507; His kinase.

"InterPro; IPR008207; His kina."

"InterPro; IPR008207; His kina."

"InterPro; IPR008207; His kina."

"InterPro; IPR008104; PAS.

"InterPro; IPR008107; His kina."

"InterPro; IPR008107; His kina."

"InterPro; IPR008107; His kina."

"InterPro; IPR008207; His kina."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=PA14;
PubMed=14983043;
He J. Baldini R.L., Deziel E., Saucier M., Zhang Q., Liberati N.T.,
Lee J., Urbach J., Goodman H.M., Rahme L.G.;
"The broad host range pathogen Peeudomonas aeruginosa strain PA14
carries two pathogenicity islands harboring plant and animal virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2004 (TrEMBLrel. 26, Last annotation update)
AGTRAP protein.
Homo sapiens (Human)
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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Promo, PD000039; Response_reg; 1.
Probom, PD000039; Response_reg; 1.
SWART; SW00387; HAFBase c; 1.
SWART; SW00388; HisKA; 1.
SWART; SW00389; HisKA; 1.
SWART; SW00448; REC; 1.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50110; RESPONSE_REGULATORY; 1.
ROSITE; PS50110; RESPONSE_REGULATORY; 1.
Kinase; Phosphorylation; Sensory transduction; Transferase.
SEQUENCE 1084 AA; 119129 MW; C953FDD2F273BFIB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.7%; Score 43; DB 2; Length 1084; 66.7%; Pred. No. 6e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                 PRT; 1084 AA
                                                                                                                                       Created)
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                                                                                                                        01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                           ORFNames=RL038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 66.7
Matches 6, Conservative
                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                750 GAWLKAWGC 758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=287;
                                                                                                                                                                                                                                                                           Name=rcsC;
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                                                                                               Q7WY20;
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RESULT 13
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PRELIMINARY; PRT; 159 AA.
OBORW9;
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-OCT-2000 (TrEMBLrel. 26, Last annotation update)
ATRAP.
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Bubaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE FROM N.A.
YE R.D., He R.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFL65187; AAF89547.1; -.
Genew; HGNC:1353, AGTRAP.
InterPro; IPR009436; AGTRAP.
Pfam; PF06396; AGTRAP; 1.
SEQUENCE 159 AA; 17518 MW; 78012C7B79AE6BC5 CRC64;
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1 cgywltiwgc 10 score: Sequence: Title: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 2002273 segs, 358729299 residues Searched:

444336

Minimum DB seq length: 0

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_23Sep04:* Database

geneseqq1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2001s:* geneseqp2003s:* geneseqp20048:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Abp53932 VEGFR-3 b	Abp53931 VEGFR-3 b	Abp53968 VEGFR-3 b	Abj04472 Stem cell	Stem	Abj04460 Stem cell	Abj04531 Molt-4 le	Abp53964 VEGFR-3 b	Aay03715 Fluorine-	Aay76817 Immunogen	•	Adg94005 Immunogen		_	Abb46607 Desmocoll			Abp22609 HIV A11 m	_	Aau90543 Insulin/i	Aau90464 Insulin/i	Aau90542 Insulin/i	Aau90541 Insulin/i	Aaw43886 Specific	Aay66209 HLA-A3-bi
ID	ABP53932	ABP53931	ABP53968	ABJ04472	ABJ04461	ABJ04460	ABJ04531	ABP53964	AAY03715	AAY76817	ABP53965	ADG94005	ADL98014	ABB46346	ABB46607	AAY76794	ABP53418	ABP22609	ABP20314	AAU90543	AAU90464	AAU90542	AAU90541	AAW43886	AAY66209
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% Query Match	100.0	75.0	69.4	54.9	49.3	48.6	46.5	45.8	45.8	45.8	45.8	45.8	45.8	45.8	45.8	44.4	44.4	44.4	44.4	44.4	44.4	44.4	44.4	44.4	44.4
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ALIGNMENTS

angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotennive; antidiabetic; unnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypottension; post-trauma; chronic hepatitis; haemangioma; diabetes; pDGF; platelet derived growth factor. Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; VEGFR-3 binding peptide SEQ ID NO:35. ABP53932 standard; peptide; 10 AA (first entry) 09-JAN-2003 ABP53932; RESULT 1 ABP53932

WO200257299-A2. sapiens. 25-JUL-2002. Synthetic. Ношо

17-JAN-2001; 2001US-0262476P. 16-JAN-2002; 2002WO-IB000099.

(LUDW-) LUDWIG INST CANCER RES. (LICN) LICENTIA LTD.

Kubo H; Alitalo K, Koivunen E,

WPI; 2002-691521/74.

New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.

Claim 13; Page 80; 149pp; English.

The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

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                                      ovary,
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                        pancreas, colon, stomach, breast, endometrium, prostate, testicie, ovary skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangionas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
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spleen, kidney, lymph node, small intestine, blood cells
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                                                                                                                                                                                                                                                                                                                                 100.0%; Score 72; DB 5; Length 10; 100.0%; Pred. No. 0.0025; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, marrow or blood, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
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                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                             75.0%; Score 54; 100.0%; Pred. No.
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                                                                                                                                                                                             Local Similarity
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                                                                                                              present invention
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The invention comprises a method (BRASIL - Biopanning and Rapid Analysis of Selective Interactive Ligands) to obtain a targeting peptide. The BRASIL method of the invention involves: exposing a target to a phage display library in a first phase; exposing the first phase to a second phase; and separating the phage bound to the target from unbound phage. The BRASIL method of the invention allows cell phages to be separated from the remaining unbound phage in a single differential centrifugation method shows a significant increase in recovery of specific phage and a substantial decrease in background. The BRASIL method is useful for method shown as a significant increase in recovery of specific phage and a substantial decrease in background. The BRASIL method is useful for method of the invention are useful for tracting peptides identified by the method of the invention are useful for treating disease states, such as diseases; bacterial infection; viral infection; cardiovascular disease and
                             pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemanjomas and diabetes. The present sequence represents a VEGFR-3 binding peptide, which is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BRASIL; targeting peptide; bacterial infection; biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes; inflammatory arthritis; atheroscalerosis; cancer; autoimmune disease; viral infection; cardiovascular disease; degenerative disease
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                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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liver, spleen, kidney, lymph node, small intestine, blood cells,
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Pred. No. 2.3;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200220822-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABJ04472;
                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arap W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABJOHATTA ABJOHA
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The invention comprises a method (BRASIL - Biopanning and Rapid Analysis of Selective Interactive Ligands) to obtain a targeting peptide. The BRASIL method of the invention involves: exposing a target to a phage display library in a first phase; exposing the first phase to a second phase; and separating the phase; exposing the first phase to a second from the BRASIL method of the invention allows cell phages to be separated from the remaining unbound phage in a single differential centrifugation step. When compared to conventional cell panning methods, the BRASIL method shows a significant increase in recovery of specific phage and substantial decrease in background. The BRASIL method is useful for identifying targeting peptides. The targeting peptides identified by the method of the invention are useful for treating disease states, such as: diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune disease; bacterial infection; viral infection; cardiovascular disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identification of targeting peptides that can be used to treat diseases e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis of Selective Ligands) method comprises a single differential
                                                                                                          Gарв
                                                                                                                                                                                                                                                                                                                                                                                                               BRASIL; targeting peptide; bacterial infection;
Biopanning and Rapid Analysis of Selective Interactive Ligands; diabs
inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;
viral infection; cardiovascular disease; degenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             degenerative disease. The present amino acid sequence represents a targeting peptide of the invention
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                                                                                                        Indele
                                                                    Score 39.5; DB 5;
Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35.5; DB 5;
Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                 Stem cell (mesenchymal) targeting peptide 50
                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Page 76; 167pp; English.
of the invention
                                                                                                                                                                                                                                                                         ABJ04461 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JAN-2001; 2001US-00765101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-SEP-2001; 2001WO-US028124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-SEP-2000; 2000US-0231266P
                                                                      54.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                          6; Conservative
                                                                                                                                            10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arap W, Pasqualini R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  targeting peptide of
                                                                                                                                            1 CGYWLTIWGC
                                                                                                                                                                 CG-WFSWWGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-404697/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    centrifugation step
                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
targeting peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200220822-A2
                                    Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified.
                                                                                                                                                                                                                                                                                                                                             24-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAR-2002.
                                                                                                        Matches
                                                                                                                                                                                                                                                      ABJ04461
                                                                                                                                                                                                                                   RESULT
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ABJ04531 standard; peptide; 7 AA.
                                              ABJ0453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention comprises a method (BRASIL - Biopanning and Rapid Analysis of Selective Interactive Ligands) to obtain a targeting peptide. The BRASIL method of the invention involves: exposing a target to a phage chase; and separating the phase; exposing the first phase to a gecond phase; and separating the phase bound to the target from unbound phage. The BRASIL method of the invention allows cell phases to be separated from the remaining unbound phage in a single differential centrifugation step. When compared to conventional cell panning methods, the BRASIL method shows a significant increase in recovery of specific phage and a substantial decrease in background. The BRASIL method is useful for identifying targeting peptides. The targeting peptides identified by the method of the invention are useful for treating disease states, such as: diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune disease; bacterial infection; viral infection; cardiovascular disease and construction of the invention of the second of sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
ä
                                                                                                                                                                                                                                                                                                                                                                                                                           Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes, inflammatory arthritis; atherosclerosis; cancer; autoimmune disease; viral infection; cardiovascular disease; degenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identification of targeting peptides that can be used to treat diseases e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis of Selective Ligands) method comprises a single differential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Pred. No. 1.7e+06;
1; Mismatches 3; Indels
  Indels
7
                                                                                                                                                                                                                                                                                                                                                                                                       peptide, bacterial infection;
                                                                                                                                                                                                                                                                                                                                                           Stem cell (mesenchymal) targeting peptide 49.
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           targeting peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Page 76; 167pp; English
                                                                                                                                                                                                              ABJ04460 standard; peptide; 9 AA.
2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-2000; 2000US-0231266P.
17-JAN-2001; 2001US-00765101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-SEP-2001; 2001WO-US028124
                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
5; Conservative
                                              1 CGYWLTIWGC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pasqualini R;
                                                                                        1 CGWW-GLWPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       centrifugation step
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-404697/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TEXA ) UNIV TEXAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         BRASIL; targeting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200220822-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                            24-OCT-2002
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                                                                                                                                                                                                                                                               ABJ04460;
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Matches
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The invention comprises a method (BRASIL - Biopanning and Rapid Analysis of Selective Interactive Ligands) to obtain a targeting peptide. The BRASIL method of the invention involves: exposing a target to a phage display library in a first phase; exposing the first phase to a second phase; and separating the phage bound to the target from unbound phage. The BRASIL method of the invention allows cell phases to be separated from the remaining unbound phage in a single differential centrifugation step. When compared to conventional cell panning methods, the BRASIL method shows a significant increase in recovery of specific phage and a substantial decrease in background. The BRASIL method is useful for identifying targeting peptides in recovery of specific phage and a decrease; inflammatory arthritis; atherosclerosis; cancer; autoimmune disease; hacterial infection; viral infection; cardiovascular disease and degenerative disease. The present maino acid sequence represents a rargeting peptide of the invention
                                                                                                                            BRASIL; targeting peptide; bacterial infection; Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune disease; viral infection; cardiovascular disease; degenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identification of targeting peptides that can be used to treat diseases e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis of Selective Ligands) method comprises a single differential centrifugation step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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50.0%; Pred. No. 1.7e+06;
iive 0; Mismatches 2;
                                                                Molt-4 leukaemia cell line targeting peptide 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 79; Page 100; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP53964 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-SEP-2001; 2001WO-US028124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L7-JAN-2001; 2001US-00765101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-SEP-2000; 2000US-0231266P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TEXA ) UNIV TEXAS SYSTEM.
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arap W, Pasqualini R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                               WO200220822-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7 AA;
                                                                                                                                                                                                                                                                                                           Unidentified
   24-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP53964
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Matches
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CGYWLTIW 8

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CDWWTTAW

/note= "N-terminal acetylation; optionally has a free or protected thiol group" 2

Location/Qualifiers

Misc-difference

'note= "D-form residue" note= "D-form residue"

Misc-difference

Misc-difference

Misc-difference Misc-difference

Misc-difference

ö

/note= "D-form residue; optionally has a free protected thiol group"

note= "D-form residue" /note= "D-form residue"

98WO-US018268

3-SEP-1998; 03-SEP-1997;

WO9911590-A1 11-MAR-1999. (IMMI-) IMMINOMEDICS INC

WPI; 1999-228967/19.

Griffiths GL;

de, targeting vector; positron emission tomography; F-18; thiol; fluorine-18.

Fluorine-18 (F-18) labeled peptide 2.

18F radionuclide;

radiolabeling;

Synthetic

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) and extrostatic, hepatotropic, antiinflammatory, hypotensive, antiidabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases. The present sequence chronic hepatitis, haemangloms and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                     Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis, vascular endothelial growth factor; cytostatic; hepartorropic; antiinflammatory; hypotensive; antiidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                           /note= "X is any amino acid"
                                                   VEGFR-3 binding peptide SEQ ID NO:67.
                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 21; Page 81; 149pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kubo H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LUDW-) LUDWIG INST CANCER RES (LICN ) LICENTIA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                      16-JAN-2002; 2002WO-IB000099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JAN-2001; 2001US-0262476P.
                  09-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alitalo K, Koivunen E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-691521/74.
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                                                                                                                                                                                                                                                                                          Wisc-difference 4
                                                                                                                                                                                                                                                                                                                                               WO200257299-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7 AA;
                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                  25-JUL-2002
                                                                                                                                                                                                                                      Synthetic.
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The invention relates to a method for incorporating 18F radionuclide into peptide-containing peptides with cansaining peptides with a fadiolabeling thiol-concaining peptides with cansaining peptides with cluorine-18 (F-18) comprises reacting a peptide comprising a free thiol group with a labeling reagent of formula: 18F-(CH2)m-CRIR2-(CH2)n-X, or a comparated alkene in which at least one of the two double bonded carbon atoms beast at least one leaving group comprising I. Br. Cl. azide, cosylate, mesylate, nosylate, nosylate, mesylate, mesylate, nosylate, in mesolate, maleimide (optionally substituted by 1-2 alkyl) or 3-sulfomaleimide; Rl. Cl. azide, tosylate, mesylate, nosylate, triflate, mlending comprision of the sulfomic acid, tertiary ammonium, alkyl (optionally substituted by COOH, OH, sulfomic acid, tertiary ammonium, alkyl or gusternary ammonium, coox, COOH, OH, sulfomic acid, tertiary ammine or characternary ammonium, alkyl or phenyl: The method is used for Radiolabeling peptide-containing targeting vectors such as proteins, antibodies, antibody fragments and receptor-targeted peptides for use in routine clinical positron enission congraphy. The method is simple and efficient. The method uses the unique property of the free thiol groups which are rapidly alkylated at neutral pH and moderate temperature. Sequences AAY0314-716 represent caramples of F-18 labeled peptides in the method of detecting a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A5.8%; Score 33; DB 2; Le Similarity 100.0%; Pred. No. 1.7e+06; 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; Page 15; 22pp; English.
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Best Local Similarity
Matches 4; Conserva
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AAY03715 standard; peptide; 8 AA

GYWXXXW 7

08-JUN-1999 (first entry)

AAY03715;

RESULT 9
AAY03715
ID AAYC
XX
AC AAYC
XX

Radiolabeling thiol-containing peptides with fluorine-18.

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Gaps

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AAY76817 standard; peptide; 8 AA
                                                                                                                                                                                                                Claim 22; Page 61; 76pp; English
                                                                                                                                                                             (IMMU-) IMMUNOMEDICS INC
                                                                                                                                                                                            WPI; 2000-160561/14
                                                                                                Misc-difference 3
                                                                         Misc-difference
                                                                                         Misc-difference
                                                                                                                       Misc-difference
                                                                                                                               Misc-difference
                                                                                                        Misc-difference
CGYW
                                                                                                                                          WO9966951-A2
                                                                                                                                                         22-JUN-1999;
                                                                                                                                                                 22-JUN-1998;
                                                                                                                                                                     14-OCT-1998;
                                  28-APR-2000
                                                                                                                                                  29-DEC-1999
                                                                                                                                                                                                       conjugates
                                                                                                                                                                                     Hansen HJ,
                                                              Synthetic
                           AAY76817;
            RESULT 10
                AAY76817
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The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antiidabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oscophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, the present sequence chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                                                                                                                Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
                                                               Indels
                    Length 8;
                                                               .
0
                    DB 3; Le
1.7e+06;

    .6
    'note≈ "X is any amino acid"

                    Score 33; DB 3; Pred. No. 1.7e
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                                                                                                                                                                                                                                                                                                                                                                                            VEGFR-3 binding peptide SEQ ID NO:68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 22; Page 81; 149pp; English.
                                                                                                                                                                                                                                                             ABP53965 standard; peptide; 8 AA.
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               45.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JAN-2002; 2002WO-IB000099
Query Match
Best Local Similarity 100...
4; Conservative
                                                                                                                                                                                                                                                                                                                                                   09-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Koivunen E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention
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                                                                                                          1 CGYW 4
                                                                                                                                                     CGYW 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200257299-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                        ABP53965;
                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                           ABP53965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating or identifying diseased tissues in a patient comprising administering a bi-specific cartibody (or fragment) having at at least 1 arm (A) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targetable conjugate. The methods and bi-specific antibodies and fusion proteins are useful for pre-targetling methods of diagnosis and therapy. It is advantageous to raise bi-specific antibodies against a targetable conjugate that is capable of carrying at least 1 diagnostic or therapeutic agent or diagnostic agent can be varied to accommodate differing applications without raising new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo clearance when used within the bi-specific antibody targeting method
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "acetylated; modified with free amino acid group, protected amino acid group, chelating agent or a metal-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "D-form residue; modified with free amino acid group, protected amino acid group, chelating agent or a metal-chelate complex"
                                                                                                                                                                                                                                                                               Immunogenic peptide; bi-specific antibody; diagnosis; immune response; diseased tissue identification; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bi-specific antibodies that bind specific target tissue and targeted
                                                                                                                                                                                                                                      Immunogenic peptide for bi-specific antibody recognition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leung S, Mcbride WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "D-form residue"
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                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chelate complex"
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                                                                                                                                                                                           (first entry)
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Sequence 8 AA

Sequence 8 AA

Gaps

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Indels Length 8;

DB 7; Le

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photodynamic diagnosis; cancer; tumour; cardiovascular lesion;
inflammatory disease; neurodegenerative disease; metabolic disease;
infectious disease; B-cell malignancy; Alzheimer's disease; amyloidosis;
autoimmune disease; bacterial infection; fungal infection;
parasitic infection; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating cancer and metabolic diseases by administering a multi-specific antibody having a targeting arm that binds to an antigen and a capture arm that binds to a polymer conjugate comprising a therapeutic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method of diagnosing or treating a disease or disorder. The method involves administering to a tissue a multi-specific antibody (I) or antibody fragment, comprising a targeting arm that binds to an antigen on the target site, and a capture arm that binds to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Optionally Cysteinyl; if Cys the residue is methylated; N-terminal acetylated."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Optionally Cysteinyl; if Cys the residue is methylated; N-terminal acetylated."
                                              45.8%; Scor.
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                        carcinoembryonic antigen-expressing tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hansen HJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "D form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "D form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "D form residue"
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                                                                                                                                                                                                                         ADL98014 standard; peptide; 8 AA.
in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JUN-2003; 2003US-00456580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JUL-2001; 2001US-0308605P.
31-JUL-2002; 2002US-00209592.
                                                                                                                                                                                                                                                                                     (first entry)
                                                      Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IMMU-) IMMUNOMEDICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-313738/29.
                                                                                                                                                                                                                                                                                                                  Peptide hapten #2
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                             Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
                                                                                                                   1 CGYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
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                                                                                                                                                                                                                                                                                     20-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating
antibody 1
                                                                                                                                                                                                                                                       ADL98014;
                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                           ADL98014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to targeting an agent towards a target site in a tissue, comprising administering to the tissue, a multi-specific antibody or its fragment, comprising a targeting arm that binds to an antigen of the target site and a capture arm that binds to a polymer conjugate, and administering a polymer conjugate that binds to the capture arm, the conjugate has a polymer conjugate to the agent such as therapeutic agent, a peptide, an enzyme and a labelled ligand. Also included is a kit useful for targeting a target site within a tissue in a subject or tissue sample comprising the above mentioned multi-specific antibody or its fragment and a polymer conjugate. The method is used for targeting an agent towards a target site in a tissue (e.g. a tumour). The method is also useful for therapputic or diagnostic purposes and further in photodynamic therapy. The present sequence is an immunogenic peptide used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Targeting an agent towards a target site in a tissue, by administering in a tissue, a multi-specific antibody or its fragment and a polymer conjugate that binds to the capture arm of the multi-specific antibody.
                                                                                                                                                                                                                                                                                             peptide; multi-specific antibody; polymer conjugate; tumour; photodynamic therapy.
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "optionally methylated or Acetylated D-form
                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                         note= "Optionally methylated or Acetylated"
          Score 33; DB 5; Length 8;
Pred. No. 1.7e+06;
0; Mismatches 3; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 14; 19pp; English.
                                                                                                                                                                             ADG94005 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "D-form
          Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMMU-) IMMUNOMEDICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-801085/75.
                                                                                                                                                                                                                                                                     Immunogenic peptide
                                                                      2 GYWLTIW 8
                                                                                                  1 GYWXXXW 7
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                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
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                                                                                                                                                                                                                                      11-MAR-2004
                                                                                                                                                                                                                                                                                                                 cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-FEB-2003
                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                          ADG94005;
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Sequence 8 AA;

The solid tunour is calced hyphatic leukaenias, and multiple myeloma. The solid tunour is calcosen melanoma, carcinoma dyreferably renal carcinoma, lung carcinoma, intestinal carcinoma and stement carcinoma, of carcinoma, lung carcinoma, intestinal carcinoma is chosen from infarts. Carcinoma, lung carcinoma, intestinal carcinoma is chosen from infarts. Clot, embolus, atheroselercit plaque and ischaenia. The metabolic disease or disorder is amyloidosis, where the antibody binds amyloid. The disease or disorder is displaced or ectopic normal tissue the nethod can be used for normal tissue. The classes or disorder is displaced or ectopic normal tissue chosen from endometrium, thymus, splean and parathyroid. The method can be used for normal tissue the disease or disorder is an autoimmume disease such as muntoimmume disease or disorder is an autoimmume disease such as muntoimmume disease or disorder is displaced or ectopic normal tissue is chosen from bone marrow and splem. The upon sephritis, rhupus erythemacous, and rhematod attritis, cluss ill autoimmume diseases such as immune—mediated thrombocytopenia gravis, upons erythemacous, and paperhicis, systemic lugas and choracytopenia systemic lugas solutions. Systemia systemia synticme, thrombocytopenia erythemacous, maltiple erythemacous, systemia militiple erythemacous, systemia purpura, post-trombocytopenic purpura and choracytopenia synthemacous, systemia synthemacous, systemia, erythemacous, systemia, sy polymer conjugate, and administering to the tissue a polymer conjugate that binds to the capture arm, the polymer conjugate comprising a polymer conjugated to a diagnostic or therapeutic agent. Also included is a conjugated to a diagnostic or therapeutic agent. Also included is a dethod for photodynamic diagnosis or treatment of a disease or disorder; or intravascular or endoscopic method for diagnosing or treating a disease or disorder. The method is useful for diagnosing or treating a disease or disorder chosen from cancer (oseophageal, gastric, colonic, rectal, pancreatic, lung, breast, ovarian, urinary bladder, endometrial, cervical, testicular, renal, adrenal and liver cancer, solid tumour, B-cervical, testicular, renal, adrenal and liver cancer, solid tumour, B-cell malignancy or T-cell malignancy is catiovascular lesion; an infectious disease, neurodegenerative disease; metabolic disease; and an infectious disease. The B-cell malignancy is chosen from indolent forms of B-cell lymphomas, acute lymphatic leukaemias, and multiple myeloma. production transportant transpo

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The invention relates to modulating agents for inhibiting or enhancing desmosomal cadherin mediated cell adhesion, comprising a modulating agent comprising a deemosomal cadherin cell adhesion recognition CAR sequence (ABB45314-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR sequence, a substance such as an antibody or antigen-binding fragment that specifically binds a desmosomal cadherin CAR sequence and/or a polymorlocide encoding a polypeptide that comprises a desmosomal cadherin CAR sequence or analogue. The modulating agents have immunosuppressive, cytostatic and antiapoptotic activity and are used to facilitate wound healing and/or reduce scar tissue, for enhancing adhesion of foreign tissue implants (e.g. skin graft or organ implant), treating an autoimmune blistering disorder and to treat cancer (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                         Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive; cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft; organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modulating agents for inhibiting or enhancing desmosomal cadherin mediated cell adhesion, useful for facilitating wound healing and/or reducing scar tissue, treating cancer and inducing apoptosis.
                                   Gaps
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Pred. No. 4.6e+02;
0; Mismatches 4; Indels
                                 Indels
 Length 8;
                                                                                                                                                                                                                                                                                         Desmoglein-2 CAR sequence cyclic peptide SEQ ID NO 1090.
               1.7e+06;
45.8%; Score 33; DB 8; 100.0%; Pred. No. 1.7e+0
          100.0%; Pred. w.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 18; Page 101; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gour BJ;
                                                                                                                                                                                        ABB46346 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAR-2000; 2000US-00535852.
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                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blaschuk OW, Symonds JM,
                                   4; Conservative
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                   1 CGYW 4
                                                                                                   CGYW 8
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                                                                                                                                                                                                                                                         30-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                         ABB46346;
                                 Matches
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                                                                                                                                                      RESULT 14
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The invention relates to modulating agents for inhibiting or enhancing desmosomal cadherin mediated cell adhesion; comprising a modulating agent comprising a desmosomal cadherin cell adhesion recognition CAR sequence (ABB45314-ABB47562), a non-peptide mimetic of a desmosomal cadherin CAR sequence, a substance such as an antibody or antigen-binding fragment that specifically binds a desmosomal cadherin CAR sequence and/or a polynucleotide encoding a polypeptide that comprises a desmosomal cadherin CAR sequence or analogue. The modulating agents have immunosuppressive, cytostatic and antiapoptotic activity and are used to facilitate wound healing and/or reduce scar tissue, for enhancing adhesion of foreign tissue implants (e.g. skin graft or organ implant), treating an autoimmune blistering disorder and to treat cancer (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis
                                                                                                                                                                    Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive; cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft; organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modulating agents for inhibiting or enhancing desmosomal cadherin mediated cell adhesion, useful for facilitating wound healing and/or reducing scar tissue, treating cancer and inducing apoptosis.
                                                                                                                                 Desmocollin-1 CAR cyclic peptide 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gour BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 23; Page 109; 127pp; English.
                  ABB46607 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                       27-MAR-2001; 2001WO-IB001400.
                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-2000; 2000US-00535852.
                                                                                           30-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blaschuk OW, Symonds JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-025778/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10 AA;
                                                                                                                                                                                                                                                                                          WO200172956-A2.
                                                                                                                                                                                                                                                                                                                                  04-OCT-2001.
                                                                                                                                                                                                                                                     Synthetic.
                                                      ABB46607;
ABB46607
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Gaps ö Query Match 45.8%; Score 33; DB 5; Length 10; Best Local Similarity 60.0%; Pred. No. 4.6e+02; Matches 6; Conservative 0; Mismatches 4; Indels

1 CGYWLTIWGC 10

1 CGYATTADGC 10

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Search completed: January 3, 2005, 16:07:18 Job time : 153 secs

30

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Tue Jan

seq33.sz10.rai

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

January 3, 2005, 16:02:29 ; Search time 37 Seconds Run on:

(without alignments) 17.924 Million cell updates/sec

Title: Perfect score:

1 cgywltiwgc 10 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

478139 seqs, 66318000 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq_length: 10

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:* Датараве :

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		46			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
-1	33	45.8	10	4	US-09-535-852-1090	Sequence 1090, Ap
7	33	45.8	10	4	US-09-535-852-1352	1352,
e	30	41.7	æ	~	US-08-520-535-12	12, Ap
4	30	41.7	60	~	US-09-079-432-12	12,
ß	30	41.7	0	~	US-08-986-234-92	92,
y	30	41.7	a	4	US-09-311-784A-374	374,
7	30	41.7	6	4	US-09-790-497A-1	1, A
æ	30	41.7	10	٣	US-09-108-709-22	22,
6	30	41.7	10	4		110,
10	29	40.3	2	Н	US-07-946-237-4	4, Aj
11	29	40.3	ß	~	US-08-530-566-10	2
12	29	40.3	S	ო	US-09-195-726-10	10,
13	29	40.3	2	ო	US-09-067-755-10	10,
14	29	40.3	S	4	US-08-239-765C-4	4
15	29	40.3	7	4	US-09-069-827A-94	94,
16	29	40.3	6	4	US-09-311-784A-348	346
17	29	40.3	10	7	US-08-735-253-8	8, A
18	29	40.3	10	7	US-08-735-253-13	13
19	29	40.3	10	m	US-08-481-968A-21	21,
20	29	40.3	10	n	80-	21,
21	29	40.3	10	4	US-09-947-925A-21	21,
22	28	38.9	80	٣	US-09-315-304B-1649	1649
23	28	38.9	10	-	US-08-250-789A-119	Sequence 119, App
24	28	38.9	10	4	US-09-462-917A-73	73, 1
25	28	38.9	10	4	1	3,
56	28	38.9	10	4		ď,
27	28	38.9	10	4	US-09-790-497A-24	24,

Sequence 12, Appl Sequence 12, Appl Sequence 17, Appl Sequence 1495, Ap Sequence 1495, Ap Sequence 12, Appl Sequence 1650, Ap Sequence 1650, Ap Sequence 1887, Ap Sequence 1887, Ap Sequence 1887, Ap Sequence 28, Appl Sequence 28, Appl Sequence 24, Appl Sequence 24, Appl Sequence 27, Appl Sequence 27, Appl Sequence 28, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 28, Appl Sequence 12, Appl	
US-08-191-571-12 PCT-US95-00296-12 US-08-295-0021-12 US-09-082-279B-1495 US-09-814-1495 US-09-814-1495 US-09-315-641C-1650 US-09-315-641C-1650 US-09-350-641C-1650 US-09-350-641C-1687 US-09-350-641C-1587 US-09-51S-852-1357 US-09-51S-852-1357 US-09-620-091-42 US-09-620-091-42 US-09-620-091-42 US-09-620-091-42 US-09-620-091-42 US-09-620-091-42	
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33 33 34 34 35 35 35 36 36 36 36 36 36 36 36 36 36 36 36 36	
2.55 2.55	
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ALIGNMENTS

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
             Sequence 1090, Application US/09535852
Fatent No. 6638911
Fatent No. 6638911
FACENERAL INFORMATION:
APPLICANT: Blachuk, James M.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND EWTHODS FOR MODULATING
TITLE OF INVENTION: DESMOSOWAL CADHERIN-MEDIATED FUNCTIONS
TOWNERN FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: FastSEQ for Windows Version 4.0
ENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 4; Length 10;
Pred. No. 81;
0; Mismatches 4; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CGYWLTIWGC 10
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US-09-535-852-1090
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Sequence 1352, Application US/09535852
; Sequence 1352, Application US/09535852
; Patent No. 653911
; GENERAL INFORMATION:
 APPLICANT: Blackuk, Orest W.
 APPLICANT: Symonds, James M.
 APPLICANT: Symonds, James M.
 APPLICANT: GOUT, Barbara J.
 TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
 TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
 TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
 TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
 TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
 CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SEQ ID NO 1352
LENGTH: 10 RESULT 2 US-09-535-852-1352

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CORRESPONDENCE ADDRESS:
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Best Local Similarity
                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
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US-08-986-234-92
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TYPE: PRT
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                                                   OTHER INFORMATION: Cyclicized modulating agent comprising OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence US-09-535-852-1352
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                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/08520535
Patent No. 5817750
GENERAL INFORMATION:
APPLICANT: Rucelahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/09079432
Patent No. 585572
GENERAL INFORMATION:
APPLICANT: Rucelahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
NUMBER OF SEQUENCES: 28
                                                                                                                          Score 33; DB 4; Length 10;
Pred. No. 81;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/520,535
FILING DATE: 28-AUG-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.7%; Score 30; DB 2; I
80.0%; Pred. No. 3.8e+05;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9849
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                          Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 80.0
The A; Conservative
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                                                                                                                                                                                                                                          CGYATTADGC 10
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TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDYWL 5
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US-09-079-432-12
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Patent No. 5981706
GENERAL NO. 5981706
GENERAL NO. 5981708.
APPLICANT: Wallen, et al.
TITLE OF INVENTION: Methods for Synthesizing Heat Shock Protein Complexes FILE REPERENCE: UNME-0009-1
CURRENT APPLICATION NUMBER: US/08/986,234
CURRENT FILING DATE: 1997-12-05
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                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,432
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h Similarity 100.0%; Score 30; DB 2; Le Similarity 100.0%; Pred. No. 3.8e+05; 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                          PRICKATION DATA:
PRICKATION NUMBER: US 08/520,535
PILICATION NUMBER: US 08/520,535
PILICATION NUMBER: US 08/520,535
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGIGTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-311-784A-374
; Sequence 374, Application US/09311784A
; Patent No. 6534482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.7%;
80.0%;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 amino acids
         STREET: 43.0
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: amino acid
; TOPOLOGY: circular
US-09-079-432-12
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GENERAL INFORMATION:
APPLICANT: Cotropia, Joseph P.
TITLE OF INVENTION: (gp41) of Human Immunodeficiency Virus-1 (HIV-1) and Prognosis Ter
TITLE OF INVENTION: Detecting the Presence and Concentration of Antibodies Inhibiting
TITLE OF INVENTION: Fusion-associated Epitope (GCSGKLIC) in gp-41
FILE REPERENCE: 10586/00406
CURRENT APPLICATION NUMBER: US/09/108, 709
CURRENT FILING DATE: 1998-07-01
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROBERT REPORTS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF ANTIBODIES OF BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
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NAME/KEY: PEPTIDB
LOCATION: (1). (10)
OTHER INFORMATION: amino acids 600-609 according to the Gnann
OTHER INFORMATION: numbering system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 10;
2.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.7%; Score 30; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 110, Application US/09790497A; Patent No. 6649735; GENEAL INFORMATION: APPLICANT: De Leys, Robert
                                                                                                                                                    Sequence 22, Application US/09108709
Patent No. 6008044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                    US-09-108-709-22
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TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT PEPTIODES AND THEIR USE IN
TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
TITLE OF INVENTION: CONTAINING THEM
TITLE OF INVENTION: CONTAINING THEM
TITLE OF INVENTION: CONTAINING THEM
FILE REFERENCE: 2752-16
CURRENT FILING DATE: 2001-02-23
PRIOR PELICATION NUMBER: 09/576,824
PRIOR PELICATION NUMBER: 09/576,824
PRIOR PELICATION NUMBER: 09/146,028
PRIOR PELING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: POT/46,028
PRIOR PELING DATE: 1993-11-22
PRIOR PELING DATE: 1993-11-22
PRIOR PELING DATE: 1993-03-08
PRIOR FILING DATE: 1993-03-08
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                                                                                                        APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: Epismune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
TITLE OF INVENTION: Immune Response and Methods of Using the Same
TITLE REFERENCE: 39963-20022.01
CURRENT APPLICATION NUMBER: US/09/311,784A
CURRENT FILING DATE: 1999-05-13
FRIOR PILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: PARESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 41.7%; Score 30; DB 4; Length 9; Best Local Similarity 100.0%; Pred. No. 3.8e+05; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: HIV1 ENV 69 (peptide 25.0113)
US-09-311-784A-374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 1, Application US/09790497A; Patent No. 6649735
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.º
....nea 4; Conservative
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SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 IWGC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 IWGC 10
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US-09-790-497A-1
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LENGTH: 9
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Query Match
Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 IWGC 10
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2 VWGC 5
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US-09-195-726-10
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Sequence 10, Application US/08530566

Patent No. 5840865

GENERAL INFORMATION:
APPLICANT: Savakis, Charalambos
APPLICANT: Branz, Gerald H.
APPLICANT: Loukeris, Athanasios
TITLE OF INVENTION: Brakaryotic Transposable Element
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Masachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
  0; Indels
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                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Savakis, Charalambos

APPLICANT: Pranz, Gerald H

APPLICANT: Loukeris, Athanasios

TITLE OF INVENTION: Enkaryotic Transposable Element
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive

CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02173
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.3%; Score 29; DB 1; I
75.0%; Pred. No. 3.8e+05;
  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFPLIATION UNDERER: US/0//940,23/
FILING DATE: 19220914
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: David E. BFTOOK
REGISTRATION NUMBER: 22,592
REGISTRATION NUMBER: 22,592
REPERMICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 100. 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                       US-07-946-237-4
; Sequence 4, Application US/07946237
; Patent No. 5348874
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: AMINO ACID
; MOLECULE TYPE: peptide
US-07-946-237-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 3; Conserva
                                      7 IWGC 10
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                                                            1 IWGC 4
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2 VWGC 5
  Matches
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COMPUTER: READABLE CORNER.

MUSTION TYPE: PLOSDY GIRK
COMPUTER: INC. PLOSDY
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Conserved amino acid sequence of the TC-1 family of transposable
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0
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KAY, Brian K
FRELINGER, Jeffrey A
HYDE-DERVISCHER, Robin P
TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING
COMPLEMENTARY COMBINATORIAL LIBRARIES
                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                         Score 29; DB 3; Length 5; Pred. No. 3.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 29; DB 4; Length 5; Pred. No. 3.8e+05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIE: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                  Sequence 4 Application US/08239765C

Sequence 4 Application US/08239765C

Retent No. 669228

GENERAL INFORMATION:

APPLICANT: Savakis, Charalambos

APPLICANT: Loukeris, Athanasios

TITLE OF INVENTION: Bukaryctic Transposable Element

FILE REFERENCE: 18747/1130

CURRENT APPLICATION NUMBER: US/08/239,765C

CURRENT FILING DATE: 1994-05-09

PRIOR FILING DATE: 1992-09-14

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin version 3.1

LENGTH: 5
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ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street N.W., Suite 300
                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 94, Application US/09069827A Patent No. 6617114 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 178
                                                                                                                         Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Conservee, OTHER INFORMATION: elements US-08-239-765C-4
                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-067-755-10
  TYPE: amino acid
                                                                                                                                                                                                                7 IWGC 10
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2 VWGC 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 IWGC 10
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US-08-239-765C-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02421
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,755
FILING DATE: 27-APR-1998
CLASSIFICATION NUMBER: US 08/530,566
FILING DATE: 20-SEP-1995
FILING DATE: 09-MAY-1994
PRIOR APPLICATION NUMBER: US 08/239,765
FILING DATE: 14-SEP-1992
APPLICATION NUMBER: US 07/946,237
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARTOALY Alice O.
REGISTRATION NUMBER: 33,542
REGISTRATION NUMBER: 33,542
TELECOMMUNICATION INFORMATION:
NAME: CARTOALY Alice O.
REGISTRATION NUMBER: 33,540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/09067755
Patent No. 6225121
GENERAL INFORMATION:
APPLICANT:
APPLICANT: Franz, Gerald H.
APPLICANT: Franz, Gerald H.
APPLICANT: Klinakis, Abostolos G.
TITLE OF INVENTION: Bukaryotic Transposable Element
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
               FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARTOIL, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: IMBB92-012AZ
TELECOMUNICATION INFORMATION:
TELEFAX: (781) 861-6240
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
APPLICATION NUMBER: US 07/946,237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ...o Militia D
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-195-726-10
                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 IWGC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VWGC 5
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US-09-067-755-10
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/069,827A
FILING DATE: 30-Apr-1998
CLASSIFICATION NUMBER: US 09/050,359
FILING DATE: 31-MAR-1998
FILING DATE: 31-MAR-1998
FILING DATE: 31-CT-1996
FILING DATE: 31-OCT-1996
FREFERENCE/DOCKET NUMBER: P8.00E
FREFERENCE/DOCKET NUMBER: P8.00E
FREFERENCE/DOCKET NUMBER: P0MLKES=4C
FELECOMUNICATION INCORMATION:
FELEPHONE: (202) 628-197
FELEPHONE: (202) 73-73-28
FRANDEDHES: single
FYPE: anino acid
FYPE: popicie
FRANDEDHESS: single
FORMATION: SEQ ID NO: 94:
FRANDEDHESS: single
FORMATION: SEQ ID NO: 34:
FRANDEDHESS: Single
FORMATION: SEQ ID NO: 38-64-05;
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FORMATION: WASHING SEQ ID NO: 38-64-05;
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FORMATION: WASHING SEQ ID NO: 38-64-05;
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Search completed: January 3, 2005, 16:11:56 Job time : 38 secs

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Sequence 104, App Sequence 185, App Sequence 174, App Sequence 176, App Sequence 107, App Sequence 107, App Sequence 186, App Sequence 187, App Sequence 188, App Sequence 188, App Sequence 188, App Sequence 188, App Sequence 189, App Sequence 180, App Sequence 180, App Sequence 180, App Sequence 181, App Sequence 21, App Sequence 2

Sequence:

Run on:

Searched:

Database

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Sequence 35, Application US/10046922

Sequence 35, Application US/10046922

Sequence 35, Application US/20020164667A1

GENERAL INFORMATION:

APPLICANT: Alitalo, Kari

APPLICANT: Kubo, Hajime

TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS

FILE REPRENCE: 2896/373084A

CURRENT FILIATION NUMBER: US/10/046,922

CURRENT FILIATION DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin version 3.0

SEQ ID NO 35

LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 72; DB 13; Length 10; 100.0%; Pred, No. 0.0026; Live 0; Mismatches 0; Indels
            US-09-894-018-185
US-09-894-018-185
US-10-371-69-374
US-10-371-65-374
US-10-371-669-374
US-10-371-669-374
US-10-371-669-374
US-10-371-645-374
US-10-371-645-374
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US-10-371-65-374
US-10-31-60-374
US-10-371-65-348
US-10-371-669-348
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; ORGANISM: isolated peptide
US-10-046-922-35
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Sequence 73, Appl
Sequence 67, Appl
Sequence 68, Appl
Sequence 1152, Ap
Sequence 1152, Ap
Sequence 39, Appl
Sequence 69, Appl
Sequence 69, Appl
Sequence 69, Appl
Sequence 15, Appl
Sequence 154, Appl
Sequence 178, Appl
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Published Applications Ast.

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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DBB sequiengthis 10 min
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US-10-046-922-68

Sequence 68, Application US/10046922

Publication No. US20020164667A1

GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Kubo, Hajime
ITILE OF INVERTION: VEGRE.3 INHIBITOR MATERIALS AND METHODS
FILE REPERENCE: 28967/37084A

CURRENT APPLICATION NUMBER: US/10/046,922

CURRENT FILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin version 3.0

LENGTH OF OF SECTION OF SECT
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS FILE REFERENCE: 28967/37084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 67
LENGTH: 7
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Publication No. US20040229811A1
GENERAL INFORMATION:
APPLICANT: Blachuk, Orest W.
APPLICANT: Blachuk, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.4977C10
CURRENT APPLICATION NUMBER: US/10/654,578
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OTHER INFORMATION: X at position 4-6 is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 13; L. Pred. No. 1.5e+06; 0; Mismatches 3;
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ORGANISM: peptide
FEATURE:
NAME/KEY: SITE
LOCATION: (4)..(6)
OTHER INVENTATION: X is any amino acid
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OTHER INFORMATION: X is any amino acid
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Best Local Similarity 57.1%;
Matches 4; Conservative (
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Matches 4; Conservative
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                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: peptide
FEATURE:
NAME/KEY: SITE
LOCATION: (4)..(6)
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US-10-654-578-1090
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Sequence 73, Application US/10046922

Publication No. US20020164667A1

GENERAL INFORMATION:

APPLICANT: Alitalo, Kari

APPLICANT: Kubo, Hajime

TITLE OF INVENTION: VEGER-3 INHIBITOR MATERIALS AND METHODS

FILE REPREBREE: 28967/37084A

CURRENT FILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin version 3.0

LENGTH: 10
          APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGER-3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 2085//37084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
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NAME/KEY: SITB
LOCATION: (1) .. (1)
OTHER INFORMATION: X is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) LOCATION: (10)...(10)
; OTHER INFORMATION: X is any amino acid US-10-046-922-34
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OTHER INFORMATION: X is any amino acid
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APPLICANT: Alitalo, Kari
APPLICANT: Koivunen, Erkki
APPLICANT: Kubo, Hajime
                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: isolated peptide
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TYPE: PRT

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Sequence 39, Application US/10133210
Publication No. US20030103964A1
GENERAL INFORMATION:
APPLICANT: Delisi, Charles
APPLICANT: Berzofsky, Jay
APPLICANT: Waccaro, Namalakar
APPLICANT: Waccaro, Dennis
APPLICANT: Waccaro, Dennis
APPLICANT: Wang, Zhiping
APPLICANT: Zhang, Chao
TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
TITLE OF INVENTION: COMPOSITIONS THEREOF
FILE REFERENCE: BU-035AX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-10-133-210-39
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Pred. No. 6.8e+02;
0; Mismatches 1; Indels
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44.4%; Score 32; DB 14; Le
Best Local Similarity 83.3%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 1;
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CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 281
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 39
LENGTH: 10
PRIOR APPLICATION NUMBER: 08/347,610
PRIOR FILING DATE: 1994-12-01
PRIOR PELING DATE: 1994-12-01
PRIOR PILING DATE: 1994-01-25
PRIOR FILING DATE: 1994-01-25
PRIOR PILING DATE: 1993-01-29
PRIOR PILING DATE: 1993-01-08
PRIOR FILING DATE: 1993-08-06
PRIOR FILING DATE: 1993-08-06
PRIOR FILING DATE: 1993-08-06
PRIOR FILING DATE: 1993-08-07
PRIOR PILING DATE: 1993-08-07
PRIOR PILING DATE: 1993-08-07
PRIOR PILING DATE: 1992-08-07
SOFTWARE: PARENTING DATE: 1992-08-07
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Publication No. US20030103964A1
GENERAL INFORMATION:
APPLICANT: DeLisi, Charles
APPLICANT: Berzofsky, Jay
APPLICANT: Gulukota, Kamalakar
APPLICANT: Vaccaro, Dennis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.4%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s LTIWGC 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-133-210-39
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US-10-133-210-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Cyclicized modulating agent comprising OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: Cyclicized modulating agent comprising
OTHER INFORMATION: desmoglein-2 cell adhesion recognition sequence
US-10-654-578-1090
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Publication NO. US20040229811A1

GENERAL INFORMATION:

APPLICANT: Blachuk, Orest W.

APPLICANT: Symonds, James Matthew

APPLICANT: Gour, Barbara J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING

TITLE OF INVENTION: DESMOSOWAL CADHERIN-MEDIATED FUNCTIONS

TITLE OF INVENTION: DESMOSOWAL CADHERIN-MEDIATED FUNCTIONS

CURRENT APPLICATION NUMBER: US/10/654,578

CURRENT FILING DATE: 2003-09-03

NUMBER OF SEQ ID NOS: 2009

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 45.8%; Score 33; DB 17; Length 10; Best Local Similarity 60.0%; Pred. No. Se+02; Matches 6; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                   45.8%; Score 33; DB 17; Length 10; 60.0%; Pred. No. 5e+02; tive 0; Mismatches 4; Indels
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APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Gste, Howard M.
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding Peptides and Their Uses
FILE REFERENCE: 206,0050000
CURRENT APPLICATION NUMBER: 08/08/821,739A
CURRENT FILING DATE: 1999-03-20
PRIOR APPLICATION NUMBER: 08/589,107
PRIOR PILING DATE: 1996-03-21
PRIOR PLING DATE: 1996-07-12
PRIOR PLING DATE: 1996-07-12
PRIOR FILING DATE: 1996-05-26
                                  NUMBER OF SEQ ID NOS: 2009
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-821-739A-90
; Sequence 90, Application US/08821739A
; Publication No. US20020168374A1
; GENERAL INFORMATION:
             2003-09-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60.0'
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             CURRENT FILING DATE:
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                                                                                  SEQ ID NO 1090
LENGTH: 10
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                                                                                                          Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Grey, Howard M.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Clis, Setteban
TITLE OF INVENTION: HLA Binding Peptides and Their Uses
FILE REFERENCE: 2060.005000A
CURRENT FILIAGO DATE: 1999-03-20
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Sequence 104, Application US/09832723

Sequence 104, Application US/09832723

Sequence 104, Application US/09832723

Sequence 104, Application US/09832723

APPLICANT: Estell, David A.

APPLICANT: Chen, Yiyou

APPLICANT: Mirray, Christopher J.

APPLICANT: Tijerina, Pilar

TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING

FILE REFERENCE: GG617-2

CURRENT PELICATION NUMBER: US/09/832,723

CURRENT PILING DATE: 2001-04-11
                                                                                                   Score 31; DB 10;
Pred. No. 9.3e+02;
                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/013, 9320 PRIOR FILING DATE: 1996-03-20 PRIOR FILING DATE: 1996-03-21 PRIOR FILING DATE: 1996-03-21 PRIOR PELING DATE: 1996-07-12 PRIOR PELING DATE: 1996-07-12 PRIOR APPLICATION NUMBER: 08/451,913 PRIOR PILING DATE: 1995-05-26 PRIOR PELING DATE: 1995-05-26 PRIOR PELING DATE: 1993-11-20 PRIOR PELING DATE: 1993-11-29 PRIOR PELING DATE: 1993-11-29 PRIOR PELING DATE: 1993-11-29 PRIOR PILING DATE: 1993-11-29 PRIOR PILING DATE: 1993-03-06 PRIOR PILING DATE: 1993-03-06 PRIOR PILING DATE: 1993-03-06 PRIOR PILING DATE: 1993-03-05 PRIOR PRIOR PILING DATE: 1993-03-05 PRIOR PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 78, Application US/08821739A Publication No. US20020168374A1 GENERAL INFORMATION:
; OTHER INFORMATION: in this patent. US-09-572-404B-1454
                                                                                                   Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
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Best Local Similarity
Matches 4; Conserv
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Sequence 1454, Application US/09572404B

Sequence 1454, Application US/09572404B

PUBLICATION NO. US20030078374A1

GENERAL INFORMATION:

APPLICANT: Proteom Ltd

TITLE OF INVENTION: Complementary peptide ligands from the human genome

FILE REFERENCE: Human patent

CURRENT APPLICATION NUMBER: US/09/572,404B

CURRENT PILING DATE: 2000-05-17

NUMBER OF SEQ ID NOS: 4203

SOFTWARE: ProtPatent version 1.0

SEQ ID NO 1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
APPLICANT: Weng, Zhiping
APPLICANT: Zhang, Chao
TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
TITLE OF INVENTION: COMPOSITIONS THEREOF
FILE REPERENCE: BU-035AX
CURRENT APPLICATION NUMBER: US/10/133,210
CURRENT APPLICATION NUMBER: 202-04-26
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 69
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-10-133-210-69
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APPLICANT: Alitalo, Kari
APPLICANT: Alitalo, Kari
APPLICANT: Koivunen, Erkki
APPLICANT: Kubo, Haliane
TITLE OF INVENTION: VEGRE.3 INHIBITOR MATERIALS AND METHODS
FILE REPERENCE: 28967/37084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT PILING DATE: 2002-01-15
WUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.4%; Score 32; DB 14; Length 10; 83.3%; Pred. No. 6.8e+02;
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0; Mismatches 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 36, Application US/10046922; Publication No. US20020164667A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 83.3
Matches 5; Conservative
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ORGANISM: Homo Sapiens
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Best Local Similarity
Matches 4; Conser
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ORGANISM: peptide
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US-10-046-922-36
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PRIOR APPLICATION NUMBER: US 60/197,259
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 117
SCFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 104
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptides screened from a phage display random US-09-832-723-104
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                                                                                                                                                                                                                                                                                                                                    Query Match
41.7%; Score 30; DB 9; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GUERALI INFORMATION:

JAPPLICANT: Sette, Alessandro

APPLICANT: Sette, Alessandro

APPLICANT: Chestrut, Robert

APPLICANT: Chestrut, Robert

APPLICANT: Chestrut, Brian

APPLICANT: Baker, Denisw

APPLICANT: Baker, Denisw

APPLICANT: Bewen, Javik

TITLE OF INVENTION: MITODS AND SYSTEM FOR OPTIMIZING

TITLE OF INVENTION: MITODS AND PEPTIDES THEREBY

FILE REFERENCE: 39963-20033.00

CURRENT APPLICANTON NUMBER: US/09/894,018

FRIOR PILING DATE: 2001-06-27

PRIOR APPLICATION NUMBER: DE0/173,390

PRIOR FILING DATE: 1999-12-28

PRIOR APPLICATION NUMBER: US 60/173,390

PRIOR APPLICATION NUMBER: US 60/284,221

PRIOR PILING DATE: 2001-04-16

PRIOR FILING DATE: 2001-04-16

NUMBER OF SEQ ID NOS: 368

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 90

LENGTH: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 80, Application US/09894018; Patent No. US20020119127A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ), OTHER INFORMATION: Oligopeptide US-09-894-018-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGYWLTIW 8
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US-09-894-018-80
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Search completed: January 3, 2005, 16:22:31 Job time : 140 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

January 3, 2005, 15:54:23 ; Search time 43 Seconds (without alignments) 22.376 Million cell updates/sec

SEQ33 72 1 cgywltiwgc 10 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

283416 seqs, 96216763 residues Searched:

1102 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum-DB-seq-length: 10.5

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
	24	33.3	1	. 7	S71868	glutathione transf
7	24	33.3	10	7	A35556	hypothetical prote
ო	22			7	PT0586	
4	22	0		7	T17075	cytochrome-c oxida
ß	21	29.5	-	~	E41946	T-cell receptor ga
9	20			~	JH0253	pentapeptide
7	20	۲.		7	F41946	T-cell receptor ga
Φ	20			7	S19288	a)
ወ	19	26.4	6	8	PT0324	Ig heavy chain CRD
10	19	26.4	10	7	PT0289	ס
11	19	26.4	7	7	E49033	-cell re
12	19	ø	7	7	F49033	receptor
13	19	26.4	10	7	C41946	-cell receptor
14	18			~	JS0315	2,
15	18	25.0	10	~	PT0230	Ig heavy chain CDR
16	18	ů.	-	7	PH0923	۲
17	18	'n.	-	~	F33932	υ
18	18	25.0	-	4	S14943	3A3 leader pe
19	17	ë.		7	B53284	l recep
20	17	•		~	PT0629	T-cell receptor be
21	17	Ψ.		7	PT0637	u
22	17	ë.		~	A61068	
23	17	•		4	I79564	netical
24	17			~	PT0628	T-cell receptor be
25	17	Э.		~	PT0642	_
26	17	23.6	7	N	PT0722	_
27	17	ë.		~	PT0728	T-cell receptor be
28	17	•	7	~	8	glucuronosyltransf
29	17	23.6		7	B48394	major fat-globule

33.3%; Score 24; DB 2; Length 10;

Query Match

pev-kinin 1 - pena triacylglycerol li neuromodulatorv pe	neuromodulatory pe neuromodulatory pe T-cell receptor be	leucokinin VI - Ma leucokinin VII - M leucokinin VIII -	angiotensin-conver adipokinetic hormo T-cell receptor be	T-cell receptor be sperm-activating p	hypotrehalosemic hypertrehalosemic
PD0029 S57274 S33244	S33245 S33246 PT0724	JS0316 JS0317 JS0318	A31570 A24244 PT0634	PT0562 A60522	B33995 S08997
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23.6	23.6 23.6 23.6	23.6	73.6 73.6 73.6 73.6	23.6	23.6
17	171	17	1111	17	17
30 31 32	, w w w 1 w 4 n	36 37 88	9 6 4 4 9 6 0 1	4243	44 45

ALIGNMENTS

	RESULT 1
	glutathione transferase (EC 2.5.1.18) class mu 4 - pig (fragment) Ninterriae names distathione citransferase oldse mu 4
	C.Species: Sus scrofa domestica (domestica pig)
	C;Date: 19-Mar-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
	R;Rouimi, P; Anglade, P.; Debrauwer, L.; Tulliez, J.
	Biochem. J. 317, 879-884, 1996 Biochem. J. 317, 879-884, 1996
	A;Reference number: S71864; MUID:96332484; PMID:8760377
	A; Accession: S71868
	A;Residues: 1-10 <rou></rou>
	A;Cross-references: (VINIPOT:Q7M3E8
	C.COMMENT: A tedat live byettes-independent classes of cycosolic gidcathion classes s mitcohondrial form are known.
	C;Complex: dimer
	Appearabtion: catalyzes the nucleophilic conjugation of intracellular glutathione to a .
	Ajtatnwaj: detoxizication; xenosiorits metabolism A Note: increased hydronhilicity of GSH-conjugates facilitates their further metabolism /
	C;Superfamily: glutathione transferase
	C.Newwolds: Glanslards
	Query Match 33.3%; Score 24; DB 2; Length 10; Rest Local Similarity 100.0%; Pred. No. 9.9e+02;
	ative 0
	Qy 2 GYW 4
	Db 4 GYW 6
-	
	RESULT 2
	hypothetical protein (ODC region) - human
	C. Species: Homo sapiens (man)
	C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 30-Sep-1993
	CyAccession: A35566 The Character of the A3556 The Character of the Control of th
	4
	A, Title: Isolation and expression of a human ornithine decarboxylase gene.
	A;Reference number: A15556; MUID:90202959; PMID:2318872 A:Arcession: A15556
	A)Status: preliminary, not compared with conceptual translation
	A; Molecule type: DNA A: Peasidines: 1=10 -MOS.
	A.Cross-references: GB:J05271

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A; Molecule type: protein
A; Residues: 1-5 <UES>
A; Residues: 1-5 <UES>
C; Commental source: gut
C; Comment: This peptide increased basal tone of the circular muscle of the esophagogastr. and of the circular muscle of the gastro-intestinal junction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: F41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R. Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: F41946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Anguilla japonica (Japanese eel)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
C;Accession: JH0253
R;Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
Biochem: Biophys. Res. Commun. 180, 828-832, 1991
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.
A;Reference number: JH0253; MUID:92062113; PMID:1953755
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C;Species: Kluyvera cryocrescens
C;bate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: 519288
R;Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T-cell receptor gamma chain (1a.27) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
                                                                                                                                                                                                                                         Gaps
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                              not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 27.8%; Score 20; DB 2; Length 5; Best Local Similarity 66.7%; Pred. No. 2.8e+05; Matches 2; Conservative 1; Mismatches 0; Indels
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Pred. No. 2.8e+05; 
1; Mismatches 2; Indels
                                                                                                                                                                            Length 10;
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Pred. No. 2.8e+03;
1; Mismatches 2;
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Similarity 40.0%;
2; Conservative 1
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                                                                                                                                                                                                       Best Local Similarity 40.0 Matches 2; Conservative
A;Accession: B41946
A;Status: preliminary; not c
A;Molecule type: DNA
A;Residues: 1-10 cMHES
C;Keywords: T-cell receptor
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Best Local Similarity
Matches 2; Conserv
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1 GFW 3
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T-cell receptor gamma chain (la.9) - mouse (fragment)
C;Speciaes: Mus musculus (house mouse)
C;Speciaes: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: E41946
C;Accession: E41946
Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R. Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge A;Reference number: A41946; MUID:92049316; PMID:1658619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
T17075
Cytochrome-c oxidase (EC 1.9.3.1) chain I - Chamaeleo fischeri mitochondrion (fragment)
C;Species: mitochondrion Chamaeleo fischeri
C;Species: mitochondrion Chamaeleo fischeri
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997
J. Mol. Evol. 44, 660-674, 1997
A;Title: Evolutionary shifts in three major structural features of the mitochondrial gen A;Reference number: Z18674; MUID:97315309; PMID:9169559
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A;Cross-references: UNIPROT:079912; EMBL:U82688; NID:g3603112; PID:g3603115; PIDN:AAC622
                                                                                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0586; PT0592
S;Fecency, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 <FES.
A;Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)
C;Keywords: T-cell receptor
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Pred. No. 2e+03;
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                                    Indels
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         Pred. No. 9.9e+02;
0; Mismatches 1;
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A;Molecule type: DNA
A;Residues: 1-10 <MAC>
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C;Keywords: mitochondrion; oxidoreductase
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60.0%;
         75.0%;
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Best Local Similarity 60.0
Matches 3; Conservative
                                    3; Conservative
      Best Local Similarity
Matches 3; Conserv
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T-cell receptor gamma chain (1t.60) - mouse (fragment)

C.Species: Mus musculus (house mouse)

C.Species: Mus musculus (house mouse)

C.Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C.Accession: C41946

R.Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell 11, 5902-5909, 1991

A.Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ger A.Reference number: A41946; MUID:92049316; PMID:1658619
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C,Accession: E49033; D49033
R;Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.
Eur. J. Immunol. 21, 2999-3007, 1991
Fur. J. Immunol. 11, 2999-3007, 1991
A;Title: Functionally distinct subsets of human gamma/delta T cells.
A;Reference number: A49033; MUID:92083926; PMID:1684157
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A;Title: Functionally distinct subsets of human gamma/delta T cells.
A;Reference number: A49033; MUID:92083926; PMID:1684157
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C;Date: 19-Dec-1993 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: F49033
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                                                                                                                                                                               A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-10 AMOR>
A;Cross-references: GB:S72587; NID:g240696; PIDN:AAB20630.1; PID:g240697
A;Note: sequence extracted from NCBI backbone (NCBIN:72591, NCBIP:72595)
A;Accession: D49033
                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-10 <MOR2>
A;Cross-references: GS:S72587; NID:g240696; PIDN:AAB20630.1; PID:g240697
A;Note: sequence extracted from NCBI backbone (NCBIN:72587, NCBIP:72589)
C;Keywords: T-cell receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 26.4%; Score 19; DB 2; Length 10; Best Local Similarity 50.0%; Pred. No. 5.4e+03; Matches 2; Indels Matches 2; Indels
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Pred. No. 5.4e+03;
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50.0%;
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Best Local Similarity 50.0
Matches 2; Conservative
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Best Local Similarity
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A; Residues: 1-10 < MOR>
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A, Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CALW 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain CRD3 region (clone J2-106C) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0324
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0222; MUID:91108337; PMID:1899102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Homo sapiens (man)
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C; Accession: PT0289
R; Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
A; Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
A; Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A; Reference number: PT0222; WUID:91108337; PMID:1899102
A;Title: Chemical modification of serine at the active site of penicillin acylase from A;Reference number: S19288; MUID:92109664; PMID:1764029 A;Accession: S19288
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C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 25-Aug-1995 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                               Query Match 27.8%; Score 20; DB 2; Length 8; Best Local Similarity 40.0%; Pred. No. 2.8e+05; Matches 2; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain CRD3 region (clone 4-109) - human (fragment) C;Species: Homo sapiens (man) C;Date: 30-Sep-1993 #text ch.
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Best Local Similarity 33.3%; Pred. No. 5.4e+03;
Matches 2; Conservative 3; Mismatches 1;
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A,Residues: 1-10 «YAM»
A,Experimental gource: B lymphocyte
C,Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Experimental source: B lymphocyte
                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q7M124
                                                                                                                                                      A;Molecule type: protein
A;Residues: 1-8 <MAR>
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A, Residues: 1-9 < YAM>
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                                                                                                                            A; Status: preliminary
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PT0289
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E49033
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Cispecial: Investing the control of 
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30.Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0230
R;Yamada, M: Wasserman, R:; Reichard, B.A.; Shane, S:; Caton, A.J.; Rovera, G.
R;Yamada, M: Wasserman, R:; Reichard, B.A.; Shane, S:; Caton, A.J.; Rovera, G.
A;Tritle: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Recession: PT0230
A;Residues: DNA
A;Residues: 1-10 <YAM>A;Residues: low.ce: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin
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Best Local Similarity 60.0%; Pred. No. 7.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.0%; Score 18; DB 2; Length 8; Best Local Similarity 37.5%; Pred. No. 2.8e+05; Matches 3; Conservative 1; Mismatches 4; Indels
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: January 3, 2005, 16:11:14
Job time : 45 secs
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JS0315
leucokinin V - Madeira cockroach
2; Conservative
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ITIFG 7
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                                                                                           1 CGYW 4
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PT0230
    Matches
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LABA JATMU
LABA JATMU
AC P13270
DT 01-JAN
DT 01
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Q8SHF6
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Q8sh11 bradypodion
Q61197 neisseria g
Aas16521 neisseria g
Q85db0 lepilemur s
Q85db0 lepilemur e
Q94nb0 microcebus
Q94nb1 microcebus
Q94nb1 microcebus
Q94nb1 microcebus
Q94nb1 microcebus
Q94nb2 microcebus
Q94nb2 microcebus
Q94nb2 microcebus
Q98nb3 brookesia t
Q88h83 brookesia t
Q88h89 brookesia t
Q88h89 brookesia t
Q88h96 brookesia t
Q88h96 brookesia s
Q88h96 brookesia s
Q88h96 brookesia s
Q88h96 brookesia s
Q88h96 chanaeleo w
Q88h67 chamaeleo w
Q88h67 chamaeleo r
Q88h68 chamaeleo r
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Q8shf6 chamaeleo m
Q70y57 fuerstia af
Cad45547 fuerstia
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                                                                                                                                 ; Search time 185 Seconds (without alignments) 31.101 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                   2971
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                       1825181 segs, 575374646 residues
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088HF6
070 V57
070 V51
070 
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Maximum Match 100%
Listing first 45 summaries
                                                                                       - protein search, using sw model
                                                                                                                                 January 3, 2005, 15:53:53
                                                                                                                                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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Match Length DB
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MaximummDBmseq@length: 10
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                                                                                         OM protein
                                                                                                                                                                                                                                                                        Sequence:
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Mitochondrion.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.
NCBI_TaxID=179915;
                                                                                                                  Jatropha multifida (Physic nut).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I; Malpighiales, Euphorbiaceae, Crotonoideae, Jatropheae,
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Pred. No. 5.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct protein sequencing.
SEQUENCE 10 AA; 1089 MW; D98AAD6362D1B362 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Cytochrome c oxidase subunit I (Fragment).
                                   01-07NV-1990 (Rel. 13, Created)
01-07NV-1990 (Rel. 13, Last sequence update)
05-0UL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 AA.
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2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Matches 5; Conserv
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                                                                                                                                                                                                                     NCBI_TaxID=3996;
                                                                                                                                                                                                                                                                                 TISSUE=Latex;
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Fuerstia africana.
Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.
                                                                                                                                                            SEQUENCE FROM N.A.
Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
"Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
based on three plastid DNA regions.";
Mol. Phylogenet. Evol. 31:277-299(2004).
EMBL, AJ506427, CAD45547.1;
Chloroplast; Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roulmi P., Anglade P., Debrauwer L., Tulliez J.;

"Characterization of pig liver glutathione S-transferases using HPLC-
electrospray-ionization mass spectrometry.";

Biochem. J. 317:879-884 (1996).

Bris, S71868; S71868.

GO; GO:0004364; F:glutathione transferase activity; IEA.

NON TER.
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Q7M3E8;
Q7M3E9;
Q7M3E9;
01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Sus scrofa domestica (domestic pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.3%; Score 24; DB 2; Length 10; 100.0%; Pred. No. 4.8e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 36.1%; Score 26; DB 2; Length 8; 100.0%; Pred. No. 1.8e+06; tive 0; Mismatches 0; Indels
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10 AA; 1223 MW; 5E16395AB36B5877 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-GCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytochrome c oxidase subunit I (Fragment).
                                                                                                                                                                                                                                                                                                                                                                            8 AA; 916 MW; DABEAB58637041B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bradypodion tavetanum (Dwarf Fischer's chameleon).
Mitochondrion.
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nes 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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EMBL, AJ505427; CAD45547.1; CAD45547.1; CO, GO:0003735; F:structural constituent of ribosome; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.
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                                                          Townsend T., Larson A.; "Modern transport to the "Molecular phylogenetics and mitochondrial genomic evolution in the chamaeleonidae (Reptilia, Squamata)."; Mol. Phylogenet. Evol. 23:22-36(2002).
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Pred. No. 1.8e+03;
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                                                                                                                                                                                   Townsend T.M., Larson A.L.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF444675, AAL90547.1; - GO; GO:0005739; C:mitochondrion; IEA.
                                                                                                                                                                                                                                                                                                                 5E218E2733772727 CRC64;
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14-MAR-2004 (TrEMBLrel. 27, Created)
14-MAR-2004 (TrEMBLrel. 27, Last sequence update)
14-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Ribosomal protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
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                     SEQUENCE FROM N.A.
MEDLINE=22169767; PubMed=12182400;
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                                                                                                                                                                                                                                                                                                                                                        37.5%;
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SEQUENCE 10 AA; 1276 MW;
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nes 3; Conservative
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hes 4; Conservative
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                                                                                                                                                                    SEQUENCE FROM N.A.
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WLLLW 6
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RESULT CONSTRUCT CONSTRUCT

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CAD45547 ID CAD4 AC CAD4 DT 14-N DT 14-N DT 14-N

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Matches

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STRAIN=MS11;
PubMed=15084227;
Snyder L.A., Davies J.K., Saunders N.J.;
Snyder L.A., Davies J.K., Saunders N.J.;
Whicroarray genomotyping of key experimental strains of Neisseria
genorrhoeae reveals gene complement diversity and five new neisserial
genes associated with Minimal Mobile Elements.";
BMC Genomics 5:23-23 (2004).
                                                                                       Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
Neisseriaceae, Neisseria.
NCBI_TaxID=485,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 24; DB 2; Length 10;
Pred. No. 4.8e+03;
1; Mismatches 1; Indels
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Snyder L.A.S., Davies J.K., Saunders N.J.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY386266; AAS16521.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 10 AA; 1227 MW; BACCBB286379D1A6 CRC64;
20-MAY-2004 (TrEMBLrel. 27, Created)
20-MAY-2004 (TrEMBLrel. 27, Last sequence update)
20-MAY-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 33.3%;
Best Local Similarity 60.0%;
Matches 3; Conservative
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Local Similarity 57.1%;
nes 4; Conservative
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                                                                                   Neisseria gonorrhoeae.
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                                                   Nuol (Fragment).
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PubMed=15084227;
Snyder L.A., Davies J.K., Saunders N.J.;
Snyder L.A. Davies J.K., Saunders N.J.;
Microarray genomotyping of key experimental strains of Neisseria gonorrhoeae reveals gene complement diversity and five new neisserial genes associated with Minimal Mobile Elements.";
BMC Genomics 5:23-23(2004).
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                                                                                              Townsend T., Larson A.;
"Molecular phylogenetics and mitochondrial genomic evolution in the chamaeleonidae (Reptilia, Squamata).";
Mol. Phylogenet. Evol. 23:22-36(2002).
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 Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae;
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Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
Neisseriaceae, Neisseria.
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Pred. No. 4.8e+03;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                            Score 24; DB 2; Length 10;
Pred. No. 4.8e+03;
1; Mismatches 1; Indels
                                                                                                                                                                           SEQUENCE FROM N.A.
TOWNEERD T.M., Larson A.L.;
SUbmitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF444873, AAL90472.1; ---
GO; GO:0005739; C:mitochondrion; IEA.
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STRAIN=MS11;
Snyder L.A.S., Davies J.K., Saunders N.J.;
Submitted (ESP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY386266; AAS16521.1; -
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SEQUENCE 10 AA; 1327 MW; 5E2180C7336415B7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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                                                                 SEQUENCE FROM N.A.
MEDLINE=22169767; PubMed=12182400;
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                                                                                                                                                                                                                                                                                                                               33.3%;
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Matches 3; Conservative
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                 Bradypodion.
NCBI_TaxID=179888;
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SEQUENCE FROM N.A.
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2 WLSRW 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=485;
                                                                                                                                                                                                                                                                Mitochondrion.
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Q6JL97
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Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Megaladapidae; Lepilemur.
NCBI_TaxID=78584;
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Pred. No. 1.8e+06;
0; Mismatches 0; Indels
                                                                                                                                                                                               Lepilemur septentrionalis (northern sportive lemur).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitochondrion. 1

NON TER 1 1

SEQUENCE 9 AA; 1174 MW; 16C563636B5045B0 CRC64;
                                                  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytochrome oxidase subunit III (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003)
EMBL; AF224597; AAP33652.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
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RESULT 10

10 AA.

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PRELIMINARY;

AAS16521 AAS16521;

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GO; GO:0005739; C:mitochondrion; IEA
                                                        h 32.6%;
Similarity 57.1%;
4; Conservative
           Mitochondrion.
NON TER 1 1 1
SEQUENCE 9 AA; 1160 MW;
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                                                          Query Match
Best Local Similarity
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                                                                                                        3 YWLTIWG 9
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MEDilNE=21184272; PubMed=11286490;

Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;

"Molecular phylogeny of the lemur family cheirogaleidae (primates)
based on mitochondrial DNA sequences.";

Mol. Phylogenet. Evol. 19:45-56(2001).
                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
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MEDILINE=22831663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
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MEDIJINE=22281620; PubMed=12393004;
Pastorini J., Forstner M.R., Martin R.D.;
"Phylogenetic relationships among Lemuridae (Primates): evidence from mtDNA.";
                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Megaladapidae; Lepilemur.
NCBI_TaxID=122230;
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Mammalia; Eutheria; Primates; Strepsirhini; Daubentoniidae;
Daubentonia.
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9 AA; 1160 MW; D5C563636B5045A2 CRC64;
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Last annotation update)
                                                                                             Lepilemur edwardsi (Milne-Edwards's sportive lemur)
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EMBL; AF224641; AAK70615.1; -.
EMBL; AF224642; AAK70619.1; -.
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                                                                    Cytochrome oxidase subunit III (Fragment).
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Cytochrome oxidase subunit III (Fragment).
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EMBL, AF224595; AAF33644.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
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                                    Created)
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57.1%;
                              01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
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Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;
"Molecular phylogeny of the lemur family cheirogaleidae (primates)
based on mitochondrial DNA sequences.";
Mol. Phylogenet. Evol. 19:45-56(2001).
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MEDLINE-22831663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
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Mammalia, Eutheria, Primates, Strepsirhini, Cheirogaleidae,
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Pred. No. 1.8e+06;
0; Mismatches 0; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit III (Fragment)
Name-COIII;
D5C563636B5045A2 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit III (Fragment).
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EMBL, AF224637, AAK70599.1, -.
EMBL, AF224638, AAK70609.1, -.
EMBL, AF224639, AAK70607.1, -.
GO, GO:0005739, C:mitochondrion, IEA.
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NCBI_TaxID=159956;
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                                                                      [1] SEQUENCE FROM N.A. MEDIA 1286490; MEDIANE 21184272; PubMed=11286490; Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.; "Molecular phylogeny of the lemur family cheirogaleidae (primates) based on mitochondrial DNA sequences."; Mol. Phylogenet. Evol. 19:45-56(2001).
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SEQUENCE FROM N.A.
MEDILINE=22631663; PubWed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
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MEDLINE=22631663; PubWed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy lemure.";
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Mammalia, Eutheria, Primates, Strepsirhini, Cheirogaleidae,
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    Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;
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Pred. No. 1.8e+06;
0; Mismatches 0; Indels
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SEQUENCE 9 AA, 1160 MW; D5C5633636B5045A2 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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BMB; AF224630; AAK70571.1; -.
EMB!, AF224631; AAK70575.1; -.
GO: GO:0005739; C:mitochondrion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytochrome oxidase subunit III (Fragment).
Name=COII;
Microcebus murinus (Lesser mouse lemur).
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EMBL; AF224628; AAK70553.1; -.
EMBL; AF224629; AAK70567.1; -.
GQ; GO:0005739; C:mitochondrion; IEA.
Mitochondrion.
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                                                NCBI_TaxID=122231;
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MEDLINE=21396409; PubMed=11504862;
Shao R., Campbell N.J., Schmidt E.R., Barker S.C.;
Shao R., Campbell N.J., Schmidt E.R., Barker S.C.;
Increased rate of gene rearrangement in the mitochondrial genomes of three orders of hemipteroid insects.";
Mol. Biol. Wovl. 18:1828-1832 (2001).
EMBL, AR315990, AAK5283.1;
GO; GO:0005739; C:mitochondrion; IEA. Gaps Gaps 3; 'n Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Buhemiptera; Heteroptera; Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomoidea; Score 23.5; DB 2; Length 9; Pred. No. 1.8e+06; 0; Mismatches 0; Indels Score 23.5; DB 2; Length 9; Pred. No. 1.8e+06; Indels NON TER 1 1 SEQUENCE 9 AA; 1206 MW; A2C563636B5041A6 CRC64; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Tectocoris diophthalmus (cotton harlequin bug). Cytochrome c oxidase subunit III (Fragment). Name=cox3; 9 AA 0; Mismatches Search completed: January 3, 2005, 16:10:25 Job time : 186 secs PRT;

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version 5.1.6
- 2005 Compugen Ltd.
GenCore (c) 1993
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January 3, 2005, 16:11:20 ; Search time 113.6 Seconds (without alignments) 31.578 Million cell updates/sec Run on:

US-10-046-922-34 56 1 XGYWLTIWGX 10 Perfect score:

Gapop 10.0 , Gapext 0.5 **▲BLOSUM62DX** Scoring table: Sequence:

2002273 segs, 358729299 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesequ2000s:* genesequ2001s:* genesequ2002s:* genesequ2003bs:* genesequ2003bs:* A_Geneseq_23Sep04:* geneseqp1980s:* geneseqp1990s:* 12645078 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Abp53931 VEGFR-3 b	Abp53932 VEGFR-3 b	Aao26093 Fc region	0	Aab62747 Human HIV	Abu30004 Protein e	Adc97318 E. faeciu	Aae09365 Human ATP	Aae09362 Mouse ATP	Aay43544 A human M	Aae09361 Human ATP	Aae09370 Human ATP	Aae09367 Human ATP	Aae09368 Human ATP	Aae09369 Human ATP	Aae09364 Human ATP	Aae09371 Human ATP	Aae09363 Human ATP	Abp52113 Homo sapi	Pepti	Aam31901 Peptide #	Aam71604 Human bon	Human	Abg53286 Human liv	Abg41416 Human pep
SOUTHWATES	ID	ABP53931	ABP53932	AA026093	ADJ50760	AAB62747	ABU30004	ADC97318	AAE09365	AAE09362	AAY43544	AAE09361	AAE09370	AAE09367	AAE09368	AAE09369	AAE09364	AAE09371	AAE09363	ABP52113	ABB38460	AAM31901	AAM71604	AAM59071	ABG53286	ABG41416
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Aay00213 Enterococ Abp44432 E faecali Abu88460 E. faecal Abu1371 Enterococ		0417	нннн	Abo27255 ICAM-1 bi Abo27277 Humanised Abo27273 Murine 1A Abo27257 ICAM-1 bi
AAY00213 ABP43432 ABU88460 ABU13711	ADH85745 AAY00212 ABP43431 ABU88459	ABU13710 AAO26134 ADJ50801 AAR15437	ABO27261 ABO27269 ABO27263 ABO27259	ABO27255 ABO27277 ABO27273 ABO27257
222 2	2223	266 6 14 6 14 8 116 2	116 6 116 6 116 6	116 6 116 6 116 6
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ALIGNMENTS

Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor. VEGFR-3 binding peptide SEQ ID NO:34. ¥. ABP53931 standard; peptide; 10 (first entry) 09-JAN-2003 ABP53931; RESULT 1 ABP5393:

Homo sapiens. Synthetic.

'note= "any amino acid" /note= "any amino acid" Location/Qualifiers Misc-difference Misc-difference

WO200257299-A2

25-JUL-2002.

16-JAN-2002; 2002WO-IB000099.

(LUDW-) LUDWIG INST CANCER RES. (LICN) LICENTIA LTD. 17-JAN-2001; 2001US-0262476P.

Kubo H; Alitalo K, Koivunen E,

WPI; 2002-691521/74.

New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.

Claim 12; Page 80; 149pp; English.

The present invention describes an isolated peptide (I) that binds to and

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                have cytostatic, hepatotropic, antiinflammatory, hypotenaive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of necovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangionas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VGGRR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and tracting disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostetic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
  endothelial growth factor receptor 3 (VEGFR-3). (I)
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                                                                                                                                                                                                                                                                                                                  100.0%; Score 56; DB 5; Length 10; 100.0%; Pred. No. 0.077; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEGFR-3 binding peptide SEQ ID NO:35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP53932 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (LUDW-) LUDWIG INST CANCER RES. (LICN.) LICENTIA LTD.
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                                                                                                                                                                                                                                                                                                                                                          10; Conservative
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vascular
                                                                                                                                                                                                                                                                             Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin Fc region, binding; whole blood, plasma; transgenic milk; antibody response; half-life; stability; circulatory system.
liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangionas and diabetes. The present sequence represents a specifically claimed VBGFR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptides, useful as binding molecules for detecting, isolating purifying immunoglobulin Fc-region polypeptides present in a solution, for regulating or preventing an antibody response.
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Pred. No. 5.7;
2; Mismatches 2; Indels
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                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stochl M,
                                                                                                                                                                                                                                                                                                                                                    AAO26093 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 76; 152pp; English.
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                                                                                                                                                                    100.0%;
80.0%; P
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ilarity 55.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rondon IJ, Wu Q, Ley AC,
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                   Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity
Matches 5; Conserv
                                                                                                    present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                     Sequence 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                   AA026093;
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                                                                                                                                                                                                                                                                                                                    RESULT 3
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The present invention provides the protein and coding sequences for the variable regions of human monoclonal antibodies which are immunoreactive
                                                                                                                                                                                                                                                                                                                                                                                                                              with numan immunodeficiency virus-1 (HIV-1) envelope glycoprotein gpl20. These can be used in diagnosis and therapy of HIV-1 infection
                                                                                                                                                                                                                                                                                                                 immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1 in biological sample and providing passive immunotherapy to HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
  Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
envelope glycoprotein; gp120; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44, DB 4; Length 120;
Pred. No. 51;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                   Novel human monoclonal antibody immunoreactive with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein encoded by Prokaryotic essential gene #15531
                                                                                                                                                                                                 USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 51-52; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU30004 standard; protein; 474 AA.
                                                                                                                                            23-JUN-2000; 2000WO-US017327.
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25-GCT-2001, 2001US-03292P.
08-FEB-2002, 2002US-036289P.
06-MAR-2002, 2002US-0362699P.
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50.0%;
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Best Local Similarity 50.0
Matches 5; Conservative
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103 RGYWVSYWGQ 112
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                                                                                                                                                                                                                                                                         N-PSDB; AAF29048.
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                                                                                                                                                                                                                                                                                                                                               infected mammal.
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                                                                                   WO200100678-A1
                                                          Homo sapiens
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                                                                                                               04-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of evaluating sample by providing a soluble serum protein (I), one or more compounds physically associated with (I), and a (I)-binding agent that comprises a peptide that specifically binds to (I), allowing the (I)-binding agent to bind to to form a complex including one or more compounds physically associated waith (I), separating the complex from one or more components of the sample, and evaluating one or more of the physically associated compounds. The sample comprises blood or serum, or is obtained from a biopsy. The sample may also be obtained from a tumour or a region within $5 \text{ mm of a tumour.} The method is useful for detecting modulators that modulate interaction of serum protein-binding compound and serum protein and for identifying binding ligands for serum protein. The present sequence represents a serum albumin-binding peptide identified using the
                                                                                                                                                                                                                                                                                                                                                                                                                                            Evaluating sample comprising soluble serum protein by forming complex comprising serum protein and physically associated compounds using peptide ligand that specifically binds with proteins, which is separated and evaluated.
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                                                                                                                                                                                  human serum albumin; HSA; serum; blood; tumour; human
                                                                                                                                                    Human serum albumin binding peptide, Seq ID No 297
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Pred. No. 5.7;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 297; 191pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB62747 standard; protein; 120 AA.
                                                                   ADJ50760 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                  16-JUN-2003; 2003WO-US018896
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Best Local Similarity 55.0..
                                                                                                                           (first entry)
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GYWCNVWGL 9
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                                                                                                                           06-MAY-2004
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                                        RESULT 4
ADJ50760
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ID AAB6
XX
AC AAB6
XX
DT 03-P
XX
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Gaps

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the invention fractace to an isolated militarization where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated or polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting callular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway capacined for proliferation, or that inhibits callular proliferation; (8) identifying a gene required for callular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound activity, all a culture compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound activity; (11) aculture compound that inhibits the extent to which each of the strains is present in a culture or collection of proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for proliferation of an organism. The antisense mucleic acids are useful for dencing and aciditar proliferation of an organism. The aciditar proliferational aciditary proliferation of an organism. The aciditar proliferational aciditary proliferation of an organism. The aciditar proliferational aciditary proliferation of an organism. The aciditary proliferation aciditary proliferation of an organism. The aciditary proliferation aciditary proliferation of an organism to some aciditary proliferation of an organism to some aciditary proliferation aciditary proliferation of an organism to some aciditary prolif
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                                                                                                                                 screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
the target prokaryotic essential genes. Note: The sequence data for this
patent did not form part of the printed specification, but was obtained
in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                       New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine, urinary tract infection, bacteraemia, endocarditis, wound, abdominal-pelvic infection.
                                                                                                                                                                                                                                                                                      invention relates to an isolated nucleic acid comprising any
Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.6%; Score 44; DB 6; Length 474; 75.0%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                Claim 25; SEQ ID NO 57928; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E. faecium protein sequence SEQ ID 6945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADC97318 standard; protein; 492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 WGYWLTCW 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterococcus faecium
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 XGYWLTIW 8
                                                WPI; 2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                           N-PSDB; ACA33874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 474 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6583275-B1
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Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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The invention relates to an isolated nucleic acid derived from concocus faccium encoding an Enterococcus faccium polypeptide having the Enterococcus faccium polypeptide having cone of 10 fully defined sequences given in the (or comprising 40 sequential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a crecombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids are chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids is useful for diagnosing pathological conditions resulting from E. faecium bacterial infection (e.g. urinary tract infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans infection and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faecium infections. The present sequence represents one if the disclosed E. faecium proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, prenatal diagnosis, dermal lesion, cardiovascular disease, MRP6, Multidrug Resistance-associated protein 6; macular degeneration, ABCC6, ATP-binding cassette transporter, arterial insufficiency; chromosome 16; Pseudoxanthoma elasticum, PXE; heritable disorder; retinal haemorrhage;
                                                                                                                                                                                                                     New isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ATP-binding cassette transporter ABCC6, MRP6 truncated mutant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB 7; Length 492;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 6945; 243pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE09365 standard; protein; 1140 AA.
                                                                                           THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-FEB-2001; 2001WO-US005741.
98US-00107532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.6%;
75.0%;
                                    97US-0051571P
                                                    98US-0085598P
                                                                                                                                Bush D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 WGYWLTCW 118
                                                                                                                                                                     2003-799836/75.
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                                                                                                                                  Doucette-Stamm LA,
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Best Local Similarity
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                                                                                                                                                                                        N-PSDB; ADC93664,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 492 AA;
                                                                                           (GENO-) GENOME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutant; mutein.
 30-JUN-1998;
                                    02-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens.
                                                      14-MAY-1998;
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                                                                                                                                                                                                                                                                                      infection.
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Terry S;

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The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a Gysfunctions. The invention is useful for screening for the presence of a C PXE mutation. Mutations associated with PXE maps to the ATP-binding cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-co grouped into three transmembrane containing 17 membrane-spanning chalces grouped into three transmembrane domains. PXE is inherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in Skin, arteries and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial insufficiency, cardiovascular disease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE individuals in order to identify individuals with appropriate genetic counselling in view of the PXE status. The methods are useful for identifying homozygotes, compound heterozygotes or carriers and thus are useful in the area of genetic testing, carrier detection and prenatal canding nearest sequence is human ATP-binding cassette (ABC) transporter, ABCC6 (MRP6) truncated mutant which is obtained as the human ATP-hiding carrier feetived from human ATP-hiding represent PATP human ATP-hiding reserved to MRP6 protein. Note: The human ATP-hiding represented the presented represented mutant which is obtained as the human ATP-hiding represented represented represented mutant which its derived from MTP human ATP-hiding represented represented mutant and a protein for human ATP-hiding represented the presented represented mutant which its derived from MTP-hiding ATP-hiding reserved to the ATP-hiding reserved to the ATP-hiding reserved to the ATP-hiding reserved to the ATP-hiding reserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6; Multidrug Resistance-associated protein 6; macular degeneration; ABCC6; ATP-binding cassette transporter; arterial insufficiency; chromosome 16; Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage.
                                                                                                                                                                                                                                                                              Screening presence of Pseudoxanthoma elasticum mutation useful for identifying homozygotes, compound heterozygotes or carriers involves determining presence of mutation in MRP6 (ABCC6) nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse ATP-binding cassette transporter ABCC6 (MRP6) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB 4; Length 1140; Pred. No. 4.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human ATP-binding cassette transporter ABCC6 (WRP6) 3] shown in figure 3 of the specification (AAE09361)
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                                                                                                                                                   Lesaux O, Urban Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE09362 standard; protein; 1498 AA.
                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Page; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.6%;
50.0%;
                          23-PEB-2000; 2000US-0184269P
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964 RGYWLSLWAD 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 XGYWLTIWGX 10
                                                                                                                                                   Boyd CD, Csiszar K,
                                                                                                      (UYHA-) UNIV HAWAII.
                                                                                                                                                                                                     2001-536645/59
                                                                      (PXEI-) PXE INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1140 AA;
                                                                                                                                                                                                                               N-PSDB; AAD16258
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The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PKE) and PKE associated physiological dyfunctions. The invention is useful for screening for the presence of a PKE mutation. Mutations associated with PKE maps to the ATP-binding or cassette transporter ABCC6 (MRP6-Multidrug Reaistance associated protein-correct in coated in the plasma membrane containing 17 membrane spanning contosomal recessive phenotype or appears as a sporadic phenotype. PKE is autosomal recessive phenotype or appears as a sporadic phenotype. PKE is autosomal recessive phenotype or appears as a sporadic phenotype. PKE is a heritable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial lesions with associated laxity and loss of elasticity, arterial insufficiency.

Cardiovascular disease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PKE associated MRP6 alleles who are then provided with appropriate genetic individuals mine view of the PKE status. The methods are useful for counselling in view of the PKE status. The methods are useful for identifying homozygotes, compound heterozygotes or carriers and thus are useful in the area of genetic testing, carrier detection and prenatal candidangorier, ABCC6 (MRP6) protein belonging to sub-family "C". Since Resistance associated protein 6 (MRP6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapa
                                                                                                                                                                                                                                                                                                        identifying homozygotes, compound heterozygotes or carriers involves determining presence of mutation in MRP6 (ABCC6) nucleic acid.
                                                                                                                                                                                                                                                                                     Screening presence of Pseudoxanthoma elasticum mutation useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.6%; Score 44; DB 4; Length 1498; 50.0%; Pred. No. 6.1e+02; 1ve 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, MPR-related ABC transporter, MOAT protein, MOAT-E, MOAT mediated transport, anticancer drug sensitivity, transporter mediated cellular efflux; anticancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human MPR-related ABC transporter designated MOAT-E,
                                                                                                                                                                                    Terry S;
                                                                                                                                                                                  Urban Z,
                                                                                                                                                                                                                                                                                                                                                                    Example 5; Page 152-159; 163pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                    Lesaux O,
                                        23-PEB-2001; 2001WO-US005741.
                                                                              23-FEB-2000; 2000US-0184269P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%;
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959 QGYWLSLWAD 968
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                                                                                                                                                                                  Csiszar K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 1215
                                                                                                                                                                                                                          WPI; 2001-536645/59.
                                                                                                                                         (UYHA-) UNIV HAWAII
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                                                                                                                                                                                                                                             N-PSDB; AAD16236
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30-AUG-2001.
                                                                                                                      PXEI-) PXE
                                                                                                                                                                                    Boyd CD,
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Gaps ö

1; Indels

(MRP6) protein (SED ID NO:

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30-AUG-2001
                                                                                                                                                                                                               Boyd CD,
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                            Region
                                                 Region
                                                                      Region
         Region
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AAE09370
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                                                                                                                                                                                                                                                                                  The present sequence represents a human MPR-related ABC transporter (MOAT) protein, designated MOAT-B. The protein comprises a multi-domain structure including a tandem repeat of nucleotide binding folds appended C-terminal to a hydrophobic domain, having Walker A and B ATP binding sites and several potential membrane spanning domains. The MOAT nucleic acids are useful for screening a test compound for inhibition of MOAT mediated transport, indicated by restoration of anticancer drug sensitivity, which in turn causes a reduction of transporter mediated collular efflux of anticancer agents. MOAT DNA or RNA may be used as probes to detect the presence or expression of genes encoding MOAT proteins. Anti-MOAT antibodies are useful for detecting and quantitating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multidrug Resistance-associated protein 6; macular degeneration; ABCC6; ATP-binding cassette transporter; arterial insufficiency; chromosome 16; Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      656. .679
/note≈ "Nucleotide binding fold-1 (NFB-1) region"
747. .768
                                                                                                                                                                                                                                               New transporter gene useful for screening for anti-cancer drugs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ATP-binding cassette transporter ABCC6 (MRP6) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 2; Length 1503;
Pred. No. 6.1e+02;
4; Mismatches 1; Indels
                   "encoded by TGC"
                                        by TTC"
                                                                                                                                                                                                                                                                  Claim 39; Page 144-147; 153pp; English.
"encoded by ACT"
                                                                                                                                                                                             Bain L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE09361 standard; protein; 1503 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                           /note= "encoded by
                                        'note= "encoded
                                                                                                                                                                         (FOXC-) FOX CHASE CANCER CENT.
                                                                                                                       99WO-US006644.
                                                                                                                                                                                             Lee K, Belinsky M,
                                                                                                                                           98US-0079759P
98US-0095153P
                                                                                                                                                                                                                                                                                                                                                                                                                                          78.6%;
50.0%;
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964 RGYWLSLWAD 973
  note=
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         Misc-difference 1274
                            Misc-difference 1287
                                                                                                                                                                                                                WPI; 1999-610812/52
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1503 AA;
                                                                                                                                                                                                                         N-PSDB; AAZ30081
                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                   MOAT proteins
                                                                                                                       26-MAR-1999;
                                                                                                                                           27-MAR-1998;
03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                               WO9949735-A1
                                                                                                   07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE09361;
                                                                                                                                                                                           Kruh G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
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The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the ATP-binding C EXE mutation. Mutations associated with PXE maps to the ATP-binding C EXE mutation. Mutations associated with PXE maps to the ATP-binding C C assette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-c C G gene locus on chromosome IG. ABCC6 (MRP6) gene encodes a 165 kba c protein located in the plasma membrane domains. PXE is inherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterises as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial insulficiency, cardiovascular disease and retinal heamorthages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRP6 alleles who are then provided with appropriate genetic counselling in view of the PXE status. The methods are useful for connealing in view of the PXE status. The methods are useful for connealing in the part of pa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful in the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is human ATP-binding cassette (ABC)
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"Nucleotide binding fold-1 (NFB-1) region'
                                                                                                      region'
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                                                                                                note= "Nucleotide binding fold-1 (NFB-1)
                                                                                                                                                                                                                                                                                                  /note= "Nucleotide binding fold-2 (NFB-2)
                                                                                                                                                                                                 (NFB-2)
                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Nucleotide binding fold-2 (NFB-2)
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                                                                                                                                                                                                 'note= "Nucleotide binding fold-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-FEB-2001; 2001WO-US005741.
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                                                                                                                                                                                                                                                          1321.
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964 RGYWLSLWAD
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Best Local Similarity
Matches 5; Conserv
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Claim 13; Page; 163pp; English
                                                                                 23-FEB-2001; 2001WO-US005741
                                                                                         23-FEB-2000; 2000US-0184269P
19-NOV-2001 (first entry)
                                                                                                             Boyd CD, Csiszar K,
                                                                                                    (UYHA-) UNIV HAWAII
                                                                                                                    WPI; 2001-536645/59.
                                                                                                (PXEI-) PXE INT INC
                                                                                                                                                                                                                                                         Sequence 1503 AA;
                                                     Misc-difference
                                                                                                                         N-PSDB; AAD16263
                                                                 WO200162977-A2
                               mutant; mutein
                                      sapiens.
                                                                         30-AUG-2001.
                                          Synthetic.
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                                      Homo
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The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the ATP-binding cassette transporter ABCC6 (MRP6 pane encodes a 165 kDa protein located in the plasma membrane containing 17 membrane-spanning chalces grouped into three transmembrane domains. PXE is inherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in Skin, arteries and the retinal hamorrhages leading to macular cassociated laxity and loss of elasticity, arterial insufficiency, associated MRP6 alleles who are then provided with appropriate genetic candividuals in order to identify individuals with one or more PXE individuals in order to identify individuals with one or more PXE counselling in view of the PXE status. The methods are useful for counselling in view of the PXE status. The methods are useful for counselling in view of the PXE status. The methods are useful for counselling in view of the PXE status. The methods are useful for the present sequence is human ATP-binding cassette (ABC) transporter. ABCC6 (MRP6) protein. Note: The present configuration of binding cassette transporter abcc6 (MRP6) protein. Note: The present france is not shown in the specification but is derived from human ATP-figure and the sequence is not shown in the specification but is derived from human ATP-figure.
                                                                                                                                                                                                                                                                                  Human, prenatal diagnosis, dermal lesion, cardiovascular disease, MRP6, Multidrug Resistance-associated protein 6; macular degeneration, ABCC6, ATP-binding cassette transporter, arterial insufficiency; chromosome 16; Pseudoxanthoma elasticum, PXE, heritable disorder; retinal haemorrhage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Screening presence of Pseudoxanthoma elasticum mutation useful for identifying homozygotes, compound heterozygotes or carriers involves determining presence of mutation in MRP6 (ABCC6) nucleic acid.
                                                                                                                                                                                                                                 Human ATP-binding cassette transporter ABCC6 (MRP6) V1298F mutant.
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                                                            AAE09367 standard; protein; 1503 AA.
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                                                                                                                                                                          (first entry)
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N-PSDB; AAD16260.
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                                                                                                                                                                                                                                                                                                                                                                                                               mutant; mutein.
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                                                                                                                AAE09367;
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RESULT 13
AAE09367
                                                               The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a CPXE mutation. Mutations associated with PXE maps to the ATP-binding cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-or or chromosome IG. ABCC6 (MRP6) gene encodes a 165 kDa protein located in the plasma membrane containing 17 membrane-spanning helices grouped into three transmembrane domains. PXE is inherited as an cutosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in Skin, arteries and the retina, that result in dermal lesions with cassociated lastity and loss of elasticity, arterial insulficiency.

Cardiovascular disease and retinal heamorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRP6 alleles who are then provided with appropriate genetic counselling in view of the PXE status. The methods are useful for carriers and thus are useful in the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is human APP-binding cassette (ABC) transporter, ABCC6 (MRP6) R1314W mutant protein. Note: The present sequence is not shown in the specification but is derived from human ATP-binding cassette transporter ABCC6 (MRP6) protein [SED ID NO: 3] shown in figure 3 of the specification (AAE09361)
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                                                                                        Multidrug Resistance-associated protein 6; macular degeneration; ABCC6; ATP-binding cassette transporter; arterial insufficiency; chromosome 16; Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
                                                            prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
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      Human ATP-binding cassette transporter ABCC6 (MRP6) R1314W mutant.
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                                                                                                                                                                                                                                                                                                                                                                                /note= "Wild type Arg substituted with Trp"
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ŝ Terry

figure 3 of the specification (AAE09361)

5, Conservative

Best Local Similarity

Matches

:||||::| : 964 RGYWLSLWAD 973 1 XGYWLTIWGX 10

Sequence 1503 AA,

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The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the ATP-binding cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-CC 6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kba protein located in the plasma membrane domains. PXE is inherited as an elicosa grouped into three transmembrane domains. PXE is inherited as an elicosa grouped into three transmembrane domains. PXE is inherited as an elicosa grouped into three transmembrane domains. PXE is inherited as an elicosaria resistance and the retina, that result in dermal lesions with a heritable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial insufficiency, cardiovascular disease and retinal hemocrahages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRR6 alleles who are then provided with appropriate genetic counselling in view of the PXE status. The methods are useful for identifying homozygotes, compound heterozygotes or carriers and thus are
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                                                                                                                                                                                                                                                                                                                                                                                                    Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6; Multidrug Resistance-associated protein 6; macular degeneration; ABCC6; ATP-binding cassette transporter; arterial insufficiency; chromosome 16; Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                 Human ATP-binding cassette transporter ABCC6 (MRP6) G1302R mutant.
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                  Length 1503;
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                                                            1; Indels
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                    Score 44; DB 4; I
Pred. No. 6.1e+02;
4; Mismatches 1;
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                    78.6%;
50.0%;
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useful in the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is human ATP-binding cassette (ABC) transporter, ABCC6 (MRP6) G1302R mutant protein. Note: The present sequence is not shown in the specification but is derived from human ATP-binding cassette transporter ABCC6 (MRP6) protein (SED ID NO: 3) shown in figure 3 of the specification (AAE09361)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PKE) and PKE associated physiological dysfunctions. The invention is useful for screening for the presence of a PKE mutation. Mutations associated with PKE maps to the ATP-binding cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa protein located in the plasma membrane containing 17 membrane spanning helices grouped into three transmembrane domains. PKE is inherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PKE is a heritable disorder characterised by mineralisation of elastic fibers in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6; Multidrug Resietrance-associated protein 6; macular degeneration; ABCC6; ATP-binding cassette transporter; arterial insufficiency; chromosome 16; Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening presence of Pseudoxanthoma elasticum mutation useful for identifying homozygotes, compound heterozygotes or carriers involves determining presence of mutation in MRP6 (ABCC6) nucleic acid.
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ATP-binding cassette transporter ABCC6 (MRP6) A1303P mutant.
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                                                                                                                                                                  78.6%; Score 44; DB 4; Length 1503; 50.0%; Pred. No. 6.1e+02;
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                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Urban Z,
                                                                                                                                                                                                                                                                                                                                                                      AAE09369 standard; protein; 1503 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lesaux O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; Page; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-FEB-2001; 2001WO-US005741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-FEB-2000; 2000US-0184269P.
                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                      5; Conservative
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964 RGYWLSLWAD 973
                                                                                                                                                                                                                                          1 XGYWLTIWGX 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-536645/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYHA-) UNIV HAWAII
                                                                                                                                                                                   Best_Local Similarity
Matches 5; Conserv
                                                                                                                                 Sequence 1503 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boyd CD,
                                                                                                                                                                                                                                                                                                                                                                                                            AAE09369;
                                                                                                                                                                   Query Match
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skin, arteries and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial insufficiency, cardiovascular disease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRP6 alleles who are then provided with appropriate genetic counselling in view of the PXE status. The methods are useful for identifying homozygotes, compound heterozygotes or carriers and thus are useful in the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is human ATP-binding cassette (ABC) transporter, ABCC6 (MRP6) A1303P mutant protein. Note: The present sequence is not shown in the specification but is derived from human ATP-binding cassette transporter ABCC6 (MRP6) protein (SED ID NO: 3] shown in figure 3 of the specification (AAE09361)
   888888888888888888888888
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Sequence 1503 AA;

ö Gaps ö 78.6%; Score 44; DB 4; Length 1503; 50.0%; Pred. No. 6.1e+02; tive 4; Mismatches 1; Indels Query Match
Best Local Similarity 50.0%

1 XGYWLTIWGX 10 ઠે

:||||::| : 964 RGYWLSLWAD 973

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Search completed: January 3, 2005, 16:27:20 Job time : 114.6 secs

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RESULT 1
US-09-107-532A-6945
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77777777777777777
  Sequence 6945, Applisequence 9, Applisequence 3630, Applisequence 408, Applisequence 408, Applisequence 1659, Applisequence 1613, Applisequence 5, Applisequence 5, Applisequence 11, Applisequence 12, Applisequence 13, Applisequence 18, Applisequence 18, Applisequence 6560, Applis
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48006, A
4, Appli
26736, A
                                                                                                                                         January 3, 2005, 16:19:47; Search time 28.8 Seconds (without alignments) 23.027 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jescription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-107-532A-6945

US-09-792-6.16-9

US-09-792-6.16-9

US-09-134-000C-3630

US-09-134-000C-3630

US-09-248-796A-19350

US-09-248-796A-19350

US-09-240-256-2629

US-09-250-291A-191134

US-09-250-91A-191134

US-09-250-91A-191134

US-09-251-794-5

US-09-253-794-5

US-09-253-794-18

US-09-252-991A-19339

US-09-252-991A-19339

US-09-2770-767-48066

US-09-2770-767-48066

US-09-2770-767-48066

US-09-2770-767-48066
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                                                                                                                                                                                                                                                                                                                                                                                                 478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                              BLOSUM62DXe Gapoxt 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                        US-10-046-922-34
56
1 XGYWLTIWGX 10
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Match Length DB
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591
591
865
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Perfect score:
                                                                                                                                                                                                                                                                                                                                  Scoring table:
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40
38.5
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Maximum DB E
                                                                                                        OM protein
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                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
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                                                                                                                                                  Run on:
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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECTUM FOR DIAGNOSTICS AND THERAPEUTICS
                     3, Appli
                                                                              Appli
Appli
Appli
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                                                  Sequence 27334, A Sequence 15188, A Sequence 6, Appli Sequence 6, Appli
             Sequence Sequence 3
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Sequence
Sequence
Sequence
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Sequence
Sequence
                                                                                                                                                                                                         Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                  US-09-252-991A-27334
US-09-248-796A-15188
US-08-462-109A-6
US-08-462-109A-6
US-08-462-179A-6
US-08-461-384B-6
US-08-461-384B-6
US-08-461-384B-6
US-08-461-384B-6
US-08-463-092B-2
US-08-463-092B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/051571
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007:
TELEPHONE: (781)893-607:
TELEPHONE: (781)893-8277
INFORMATION FOR SEQ ID NO: 6945:
                                                                                                                                                                                          US-08-462-109A-2
US-08-462-109A-4
US-08-460-907B-2
US-08-460-907B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...492; SEQUENCE DESCRIPTION: SEQ ID NO: 6945: US-09-107-532A-6945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                              Sequence 6945, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 492 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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Page 2

**PLICANT: Gil H. Choi

TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides

**ITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides

**ITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides

**CORRESPONDENCE ADDRESS:

**ADDRESSEE: Human Genome Sciences, Inc.

**STREET: 9410 Key West Avenue

CITY: Rockville

**CONTRY: USA

ZIP: 20850

COMPITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Sequence 3630 Application US/09134000C |
| Sequence 3630 Application US/09134000C |
| Patent No. 6617156 |
| GENERAL INFORMATION: |
| APPLICANT: Lynn Doucette-Stamm et al |
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO |
| TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS |
| FILE REFERENCE: 032796-032 |
| CURRENT APPLICANTON NUMBER: US/09/134,000C |
| CURRENT FILING DATE: 1998-08-13 |
| PRIOR FILING DATE: 1997-08-15 |
| SEQ ID NOS: 6812 |
| SEQ ID NO 3630 |
| INNGTH: 229 |
| INNGTH: 220 |
| INNGTH: 
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Pred, No. 48;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.8%; Score 43; DB 4; Length 222; 50.0%; Pred. No. 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
COMPUTER: MS SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
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CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: P8369
TELEPONE: (301) 309-8504
TELEPAK: (301) 309-8512
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 76.8%;
Best Local Similarity 50.0%;
Matches 5; Conservative
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Matches 5; Conservative
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MOLECULE TYPE: protein
US-09-071-035-408
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178 AGTWITLWGQ 187
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STRANDEDNESS: sin
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US-09-134-000C-3630
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Sequence 9, Application US/09792616

Patent No. 6780587

GENERAL INFORMATION:
APPLICAMT: Winversity of Hawaii

TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
TITLE OF INVENTION: Pseudoxanthoma Elasticum
TITLE OF INVENTION NUMBER: US/09/792,616
CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT PILING DATE: 2001-02-23

NUMBER OF SEQ ID NOS: 27

SEQ ID NOS: 27

SEQ ID NOS: 27

SEQ ID NOS: 27

SEQ ID NOS: 27
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Patent No. 6780587
GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: PILE TILE TO INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing TITLE OF INVENTION: Pseudoxanthoma Elasticum
FILE REFERENCE: PXE-001
CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT PILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.6%; Score 44; DB 4; Length 1498; 50.0%; Pred. No. 2.3e+02; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                          Score 44; DB 4; Length 492;
Pred. No. 75;
                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                         1; Mismatches
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US-09-071-035-408
; Sequence 408, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
                                                                                                                                                                                                                             78.6%;
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Best Local Similarity 75.v.
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Best Local Similarity 50.0
Matches 5; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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111 WGYWLTCW 118
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                         1 XGYWLTIW 8
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TYPE: PRT
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US-09-792-616-3
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US-09-792-616-9
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Sequence 2629, Application US/09540236

Battert No. 66739101

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARF
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT PILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 2629
LENGTH: 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                     Score 41; DB 4; Length 668;
Pred. No. 2.7e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.4%; Score 40; DB 4; Length 328; 50.0%; Pred. No. 1.8e+02; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6868, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7310
                                                                                                       Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
                     ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.0
Matches 5; Conservative
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; ORGANISM: M.catarrhalis
US-09-540-236-2629
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    LENGTH:
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Patent No. 6747137
GENERAL INFORMATION:
PAPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: 611 H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Pred. No. 56;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
PRIOR PLING DATE: 1998-08-13
PRIOR PLING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: A. Andere Brookes
REGISTRATION NUMBER: 36,373
REFERENCE DOCKET NUMBER: P8369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 406:
                                                                                                                        Sequence 406, Application US/09071035
Patent No. 6448043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.8%;
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-071-035-406
: | |:|:||:
202 AGTWITLWGQ 211
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202 AGTWITLWGO 211
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                                                                                  RESULT 6
US-09-071-035-406
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67.9%;
50.0%;
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                                                                                                               4; Conservative
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Matches 4; Conservative
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16 HWLSLWGL 23
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                                                                   Query Match
Best Local Similarity
Matches 4; Conserva
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| Sequence 19134, Application US/09252991A
| Sequence 19134, Application US/09252991A
| Sequence 19134, Application US/09252991A
| Patent No. 6551795
| GENERAL INPORMATION:
| APPLICANT: Marc J. Rubenfield et al.
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
| TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
| TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: 107196.136
| CURRENT FILING DATE: 1998-02-18
| PRIOR APPLICATION NUMBER: US 60/074,788
| PRIOR APPLICATION NUMBER: US 60/094,190
| PRIOR APPLICATION NUMBER: US 60/094,190
| PRIOR FILING DATE: 1998-07-27
| NUMBER OF SEQ ID NOS: 33142
| LENGTH: 612
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 41173
LENGTH: 24
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 71.4%; Score 40; DB 4; Length 478; Best Local Similarity 62.5%; Pred. No. 2.7e+02; Matches 5; Conservative 2; Mismatches 1; Indels
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54.5%; Pred. No. 5.6e+02;
ive 3; Mismatches 1;
                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...478
SEQUENCE DESCRIPTION: SEQ ID NO: 6868:
                                                                                                             LENGTH: 478 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: unear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6868:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19134
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Best Local Similarity 54.5%,
6; Conservative
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                                                                                                                                                                                                                                                                          FEATURE:
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Us-09-270-77-11173

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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09253794

Patent No. 6676924

GENERAL INFORMATION:
APPLICANT: HANSEN, Hans J.
ARMOUR, Kathryn L.
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
MOUSE MONOCLONAL ANTIBODIES
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                                                                                                                                                                                  Score 38; DB 2; Length 119
Pred. No. 1.3e+02;
4; Mismatches 2; Indels
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Pred. No. 1.3e+02;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/253,794
FILING DATE: 22-Feb-1999
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY ARENT INFORMATION
ATTORNEY AGENT INFORMATION
NAME: SAXE, BETCHARD D. ERGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/464
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-253-794-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                Query Match
Best Local Similarity 40.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 904136
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
               INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHRAACTER.STICS:
LENGTH: 119 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 40.0°
                                                                                              MOLECULE TYPE: protein US-08-318-1578-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                : | |: : | |:
102 AGCWIDVWGQ 111
                                                                                                                                                                                                                                                           1 XGYWLTIWGX 10
904136
                                                                                        STRANDEDNESS:
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:| |: :||: 102 AGCWIDVWGQ 111

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FEATURE:

NAME/KEY: UNSURE

LOCATION: (6), (77), (85)

COTHER INFORMATION: Identity of amino acid sequences at the above locations are unknow US-09-248-796A-22785
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                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                              67.9%; Score 38; DB 4; Length 132; 85.7%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                 Search completed: January 3, 2005, 16:33:48
Job time : 29.8 secs
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85./7
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122 NGYWLTI 128
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RESULT 15
US-09-248-796A-22785
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Sequence 406, App Sequence 114, App Sequence 338, App Sequence 240891

sequence 1, Applisequence 1, Applisequence 13, Applisequence 11, Applisequence 21, Applisequence 21, Applisequence 21, Applisequence 21, Applisequence 31, Applisequence 31, Applisequence 41, Applisequence 64, Applisequence 64, Applisequence 64, Applisequence 20, Applisequence 22, Applisequence 23, A

4 US-10-206-576-406
4 US-10-125-869A-114
5 US-10-125-869A-114
6 US-09-910-483-1
0 US-09-910-483-1
0 US-09-910-483-2
0 US-09-910-483-2
0 US-09-910-483-2
0 US-09-910-483-2
0 US-09-910-483-2
0 US-09-910-483-2
0 US-09-910-483-3
0 US-09-864-761-4784
0 US-10-425-115-188067
0 US-10-425-115-188067
0 US-10-425-115-188067

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40.5
   Sequence 73, Appl
Sequence 297, App
Sequence 57928, A
Sequence 9, Appli
Sequence 9, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 43458, A
Sequence 408, App
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Sequence 35, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                      (without alignments)
35.687 Million cell updates/sec
                                                                                                                  January 3, 2005, 16:32:45; Search time 100.8 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US10P_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US10P_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US10P_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US10P_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.ppp:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-046-922-35
US-10-125-863A-73
US-10-462-262-297
US-10-282-122A-57928
US-10-437-963-190740
US-10-792-616-9
US-10-764-328-9
US-10-764-328-3
                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                        1599051 seqs, 359727711 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published_Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                      BLOSUM62DX3
Gapop 10.0:, Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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56
1 XGYWLTIWGX 10
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Match Length
                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                        Scoring table:
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                                                                                                                Run on:
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US-10-425-115-334071 US-10-276-774-1797 US-09-738-626-5178

ALIGNMENTS

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Sequence 34, Application US/10046922

Sequence 34, Application US/10046922

Bublication No. US20020164667A1

GENERAL INFORMATION:

APPLICANT: Alitalo, Kari

APPLICANT: Robo, Hajime

TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS

TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS

TITLE REPERENCE: 28967/371084A

CURRENT APPLICATION NUMBER: US/10/046,922

CURRENT PILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 80

SOFTWARE: PatentIn version 3.0

SEQ ID NO 34

LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 56; DB 13; Length 10;
100.0%; Pred. No. 0.18;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                    PEATURE:
NAME/KEY: SITE
LOCATION: (1)..(1)
OTHER INFORMATION: X is any amino acid
NAME/KEY: SITE
LOCATION: (10)..(10)
COTHER INFORMATION: X is any amino acid
US-10-046-922-34
                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: isolated peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Conservative
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Best Local Similarity
Matches 10; Conserva
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US-09-864-761-43458 US-09-071-035-408 US-10-206-576-408

1498 1503 1503 34 222

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Gaps . 0

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CURRENT PILING DATE: 2003-02-06

PRIOR APPLICATION NUMBER: 60/191, 078

PRIOR FILING DATE: 2000-03-21

PRIOR PELICATION NUMBER: 60/206, 848

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-110-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2001-12-26

PRIOR PILING DATE: 2001-12-26

PRIOR PILING DATE: 2001-12-26

PRIOR PILING DATE: 2010-12-26

PRIOR PILING DATE: 2010-12-26

PRIOR PILING DATE: 2010-12-26

PRIOR PILING DATE: 2010-02-16

PRIOR PILING 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REPRENCE: BLITRA.034A
CURRENT APPLICATION NUMBER: 105/10/282,122A
CURRENT FILING DAIR: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 55.6%; Score 44; DB 15; Length 13; Similarity 55.6%; Pred. No. 11; 5; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: immunoglobulin binding polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 57928, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Obleen, Kari
                                                       CURRENT APPLICATION NUMBER: US/10/462,262
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: US 60/388,642
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 430
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 297
LENGTH: 13
      TITLE OF INVENTION: PROTEIN ANALYSIS FILE REFERENCE: 10280-052001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GYWLTIWGX 10
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Best Local Similarity
Matches 5; Conserv
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US-10-282-122A-57928
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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RESULT 2
US-10-046-922-35

j Sequence 35, Application US/10046922

j Publication No. US20020164667A1

general Information:
   APPLICANT: Alitalo, Kari;
   APPLICANT: Kubo, Hajime
   TILLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
   TILLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
   CURRENT APPLICATION NUMBER: US/10/046,922
   CURRENT FILING DATE: 2002-01-15
   NUMBER OF SEQ ID NOS: 80
   SOFTWARE: Patentin version 3.0
   SEQ ID NO 35
   LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13, Length 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 73, Application US/10125869A
Publication No. US20030199671A1
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Wu, Qi-Long
APPLICANT: Rondon, Isaac Jesus
APPLICANT: Ley, Arthur C.
APPLICANT: Stochl, Mark
APPLICANT: Ransohoff, Thomas C.
APPLICANT: Potter, M. Daniel (deceased)
TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 3421.1006-001
CURRENT FILING DATE: 2002-11-19
CURRENT FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 200
SOFFWARE: FastSEC for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Fc region binding polypeptide US-10-125-869A-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 56; DB 1
Best Local Similarity 80.0%; Pred. No. 0.18;
Matches 8; Conservative 2; Mismatches
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Publication No. US20040009534A1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Dawson, Bruce M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: isolated peptide
US-10-046-922-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 XGYWLTIWGX 10
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US-10-125-869A-73
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LENGTH: 13
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US-09-792-616-3

Sequence 3. Application US/09792616

Sequence 3. Application US/09792616

Sequence 3. Application No. US20030165828A1

SEQUENCE NO. US20030165828A1

SEQUENCE NO. US20030165828A1

SEQUENCE NOTIVE OF Hawaii

TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing

TITLE OF INVENTION: Pseudoxanthoma Elasticum

TITLE OF INVENTION: Pseudoxanthoma Elasticum

TITLE OF INVENTION: Wubber: US/09/792,616

CURRENT FILING DATE: 2001-02-23

CURRENT FILING DATE: 2001-02-23

SOFTWARE: Patentin version 3.0

SEQ ID NO 3

LENGTH: 1503

TYPE: PRT

ORGANISM: Homo sapiens

US-09-792-616-3
                                                                                                             US-10-764-328-9

Sequence 9, Application US/10764328

Sequence 9, Application US/10764328

PUBLICATION NO. USSO040166521A1

GENERAL INFORMATION:

APPLICANT: PXE International, Inc.

APPLICANT: DIAVERSITY OF Hawaii

TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing)

TITLE OF INVENTION: Pseudoxanthoma Blasticum

FILE REFERBNCE: PXE-001PC

CURRENT APPLICATION NUMBER: US/10/764,328

CURRENT FILING DATE: 2004-01-23

NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/10764328
Publication No. US20040166521A1
GENERAL INFORMATION:
APPLICANT: PAE International, Inc.
APPLICANT: University of Hawaii
TITLE OF INVENTION: Pseudoxanthoma Blasticum
FILE REFERENCE: PXE-001PC
CURRENT APPLICANTON UNBER: US/10/764,328
CURRENT FILING DATE: 2004-01-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 16;
Pred. No. 7.4e+02;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 10;
Pred. No. 7.4e+02;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin version 3.0 sEQ ID NO 9 LENGTH: 1498 TYPE: PRT ORGANISM: Mus musculus US-10-764-328-9
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50.0%;
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50.0%;
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Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 50.0
Matches 5, Conservative
   959 QGYWLSLWAD 968
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964 RGYWLSLWAD 973
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APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT PAPLICANTON NUMBER: US/10/437,963
CURRENT PAPLICANTON NUMBER: US/10/437,963
SQUENCE OF SEQUENCE: 2003-05-14
SQUENCE OF SEQUENCE: 2003-05-14
TYPE: LENGTH: 671
TYPE: TYPE: THE OF THE OF
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Sequence 9, Application US/09792616
Sequence 9, Application US/09792616
Sequence 9, Application Wo. US20030165828A1
GENERAL INFORMATION:
APPLICANT: PXE International, Inc.
APPLICANT: University of Hawaii
TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
TITLE OF INVENTION: Peeudoxanthoma Elasticum
FILE REFERENCE: PXE-001
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Pred. No. 7.4e+02;
4; Mismatches 1; Indels 0
                                                             Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 16; Length 671;
Pred. No. 3.6e+02;
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                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT4530_87125C.1.pep
US-10-437-963-190740
                                                         Score 44; DB 15;
Pred. No. 2.7e+02;
                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                              US-10-437-963-190740
; Sequence 190740, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/792,616 CURRENT FILING DATE: 2001-02-23 NUMBER OF SEQ ID NOS: 27 SOFTWARE: Patentin version 3.0
                                                         78.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0%;
Matches 5; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                      Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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93 WGYWLTCW 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Mus musculus
US-09-792-616-9
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US-10-282-122A-57928
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Sequence 408, Application US/09071035

Publication No. US20020045737A1

GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSES: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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; FEATURE:
; OTHER INFORMATION: MAP TO AC000403.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
US-09-864-761-43458
                                                                                                                                                                                                                                                             Score 43; DB 9; Length 34; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                Indels
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...urksSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PB369P2
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 408:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION UNDBER: 36,373
                                                                                                                                                                                                                                                                76.8%;
50.0%;
                                                                                                                                                                                                                                                             Query Match 76.8
Best Local Similarity 50.0
Matches 5; Conservative
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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24 HGYWITVFGD 33
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Best Local Similarity
Matches 5; Conserva
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US-10-206-576-408
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GENERAL INPORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Fance, David R.

APPLICANT: Fance, David R.

APPLICANT: Fance, David R.

APPLICANT: Tone, Westhern G.

APPLICANT: Gree, Westhern G.

FITTER OF INVERTION: GENE EXERSISTON ANALYSIS BY MICROARRAY

CURRENT FAILE CAPITY: 200-162-23

FRIOR PLING DATE: 200-162-24

FRIOR PLING DATE
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Pred. No. 7.4e+02;
4; Mismatches 1; Indels (
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Patent No. US20020048763A1
  NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
                                                                                                                                                                                                             78.6%;
50.0%;
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Best Local Similarity 50.0.
Thea 5; Conservative
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964 RGYWLSLWAD 973
                                                                                                                                                                                                                                                                                                             1 XGYWLTIWGX 10
                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                             LENGTH: 1503
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US/09/071,035
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                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB365
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 406: SEQUENCE CHARACTERISTICS:
LENGTH: 266 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 266 amino acids
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Best Local Similarity 50.0
                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 XGYWLTIWGX 10
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TOPOLOGY: line
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             SOFTWARE:
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Sequence 408, Application US/10206576
Publication No. US20030017495A1
GENERAL INFORMATION:
APPLICANT: Choi et al.
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
STATE: Maryland
COUNTRY: USA
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US-001-035-406

Sequence 406, Application US/09071035

Publication No. US20020045737A1

GENERAL INFORMATION:

TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides

NUMBER OF SEQUENCE: 496

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA
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Pred. No. 1.9e+02;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
AMDIUM TYPE: Wettra 486/33
AMDIUM TYPE: HP Vectra 486/33
                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

COMPUTER: Dell Latitude
SOFTMARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/206,576
FILING DATE: 29-0ul-2002
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REGISTRATION NUMBER: 46,789
REGISTRATION NUMBER: 46,789
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 408:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 222 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

Best Local Similarity 50.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : | |:|:||:
178 AGTWITLWGQ 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 XGYWLTIWGX 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-206-576-408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
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Sequence 406, Application US/10206576
Publication.No. US20030017495A1
GENERAL INFORMATION:
APPLICANT: Choi et al.
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                      Gaps
                                                      ö
Score 43; DB 9; Length 266;
Pred. No. 2.2e+02;
                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

COMPUTER: Dell Latitude
COMPUTER: Dell Latitude
OPERATING SYSTEM: Windows 98
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/206,576
FILING DATE: 29-Jul-2002
CLASSIFICATION NATA:
APPLICATION NUMBER: US 09/071,035
FILING DATE: 1998-05-06
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/046,031
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/066,009
FILING DATE: 1997-01-14
ATTORNEY/ABRATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hyman, Mark J.
REGIGIRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB369PID1
INFORMATION FOR SEQ ID NO: 406:
                                                   4; Mismatches
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TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

TOPOLOGY: linear

TOPOLOGY: linear

SEQUENCE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 406:

US-10-206-576-406

Query Match
Best Local Similarity 50.0%; Pred. No. 2.2e+02;

Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 XGYWLTIWGX 10

Search completed: January 3, 2005, 16:54:14

Search completed: January 3, 2005, 16:54:14
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5.1.6
Compugen Ltd.
version 5
GenCore (c) 1993 .
        Copyright
```

- protein search, using sw model OM protein

Run on:

January 3, 2005, 16:20:13 ; Search time 22.4 Seconds (without alignments) 42.954 Million cell updates/sec

US-10-046-922-34 56 1 XGYWLTIWGX 10 score: Sequence: Perfect

_BLOSUM62DX, Gapop_10:0, Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB M

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Pred. No.

SUMMARIES

Description	probable transport	multidrug resistan	permease [imported	Ig heavy chain pre	replication protei	probable Na+/H+-ex	hypothetical prote	arginine/ornitine	probable ABC trans	na+/h+ antiporter	arginine/ornithine	probable oxidoredu	Ins P4-binding pro	Ins P4-binding pro	œ	zinc	probable integral	probable exported	ubiquinol-cytochro	hypothetical prote	rod shape-determin	ABCTransporter [im	probable transcarb	Ig heavy chain V r	hypothetical prote		protein F41H10.7 [ы	CDP-glucose 4,6-de
ID	C95307	T42216	E90446	C34903	PC4117	B71038	AF1978	C86879	C95282	C75176	T46745	T50103	S58888	S71847	A33830	JC4700	T35739	AF0881	S13868	S76385	AF1127	G90251	F82966	AVMS14	AI2232	A69843	E88690	S49164	S74751
DB	7	~	N	N	N	~	N	~	~	~	~	7	0	~	~	~	N	~	-	7	7	~	~	-	7	7	7	~	7
Query Match Length	441	1502	419	142	391	425	376	490	508	426	475	583	829	829	1063	1063	118	167	187	218	416	477	607	123	172	250	286	292	360
Query Match	78.6	78.6	9.9/	75.0	75.0	75.0	73.2	73.2	73.2	71.4	71.4	71.4	71.4	71.4	70.5	70.5	9.69	9.69	9.69	9.69	9.69	9.69	68.8	67.9	67.9	67.9	67.9	61.9	67.9
Score	44	44	43	42	42	42	41	41	41	40	40	40	40	40	39.5	39.5	39	39	39	39	39	39	38.5	38	38	38	38	38	38
Result No.		7	m	4	s	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

Ig heavy chain pre	alpha-ketoglutarat	probable amino aci	arginine/ornithine	arginine/ornitine	YSD83 protein - ye	hypothetical prote	phosphatidylglycer	hypothetical prote	hypothetical prote	1-acyl-sn-glycerol	1-acylglycerol-3-p	probable mccF prot	GP12 protein - yea	hypothetical prote	glycosyl transfera
\$12839	Н69607	E83497	JH0110	G86878	843540	F69990	E83140	AF2356	G82391	G81013	A81957	E75325	861111	A83779	D82657
7	~	~	7	~	~	~	~	~	~	7	~	~	~	7	7
380	435	472	482	497	385	164	171	197	241	247	247	257	280	292	294
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63	67	67	67	67	67	99	99	99	99	99	99	99	66.1	99	99
38	38	38	38	38	37.5	37	37	37	37	37	37	37	37	37	37
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1			
C95307	rangoort	protein	Ž.

probable transport protein SMa0684 [imported] - Sinorhizobium meliloti (strain 1021) mage C.Species: Sinorhizobium meliloti

C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

CyAccession: C95307
RyBarnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse, S. Kaalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C., Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot; A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Recession: C95307
A;Status: preliminary
A;Rocession: C95307
A;Residues: 1-441 «KUR»
A;Residues: 1-441 «KUR»
A;Residues: 1-441 «KUR»
A;Residues: 1-450-001
A;Residues: U.S. MUID:21396509; PIDN:AAK65021.1; PID:914523451; GSPDB:GFA;Residues: 1-470-001
A;Residues: 1-470-001
A;Residues: V. S. Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pela, Hyman, R.W.; Jones, T.
Const. Ryman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A;Reference number: Apronee of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Gene: SMa0684

C; Superfamily: L-lysine transport protein A;Genome: plasmid

Gaps ö Length 441; 1; Indels core 44; DB 2; 1 red. No. 25; Mismatches 1 Score 44; Pred. No. 4 78.6%; 5; Conservative Query Match Best Local Similarity Matches 5; Conserv

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1 XGYWLTIWGX 10 ઠે

:|||::|| : 91 WGYWISIWAS 100 q

RESULT 2

T42216 multidrug resistance-associated protein homolog MLP-1 - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T42216
R;Hirchashi, T.; Suzuki, H.; Ito, K.; Ogawa, K.; Kume, K.; Shimizu, T.; Sugiyama, Y.
Mol. Pharmacol. 53, 1068-1075, 1998
A;Title: Hepatic expression of multidrug resistance-associated protein-like proteins mair
A;Reference number: Z22081; MUID:98279126; PMID:9614210
A;Accession: T42216

A; Status: preliminary; translated from GB/EMBL/DDBJ

09:33:10 2005

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probable Na+/H+-exchanging protein - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Spate: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: B71038
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine
M.; Ohfuku, Y.; Punahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,,
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic and A;Reference number: A71000; MuID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-425 <KAW>
A;Cross-references: UNIPROT:059255; GB:AP000006; NID:g3236133; PIDN:BAA30706.1; PID:g3258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein alr1377 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: Nostoc sp. strain PCC 7120
C;Accession: AF1978
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Analy Reference number: AB1807; MUD: 21595285; PMID: 11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1.376 <KUR>
A;Cross-references: UNIPROT:08YX40; GB:BA000019; PIDN:BAB73334.1; PID:g17130724; GSPDB:G?
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Experimental source: strain OT3
A, Note: this accession replaces an interim accession for a sequence replaced by GenBank
replication protein homolog - Pyrococcus sp. (fragment)
NyAlternate names: hypothetical 391 protein
C;Species: Pyrococcus sp.
C;Date: 07-Peb-1996 #sequence_revision 19-Apr-1996 #text_change 17-May-1996
C;Accession: PC4117
R;Rashid, N.; Morikawa, M.; Imanaka, T.
Gene 166, 139-143, 1995
A;Title: An abnormally acidic TATA-binding protein from a hyperthermophilic archaeon. A;Reference number: JC4514; MUID:96102215; PMID:8529878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 2; Length 391;
Pred. No. 44;
1; Mismatches 1; Indels
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Pred. No. 48;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.0%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-391 <RAS>
A;Cross-references: DDBJ:D50018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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318 FGAWLTAWGR 327
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Best Local Similarity
Matches 6; Conserv
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(234903

Ig heavy chain precursor V region (5-27) - mouse
(5) Species: Mus musculus (house mouse)
(5) Species: Mus musculus (house mouse)
(7) Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996
(7) Accession: (234903
(7) Ribedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
(7) Biol. Chem. 265, 133-138, 1990
(8) A;Title: Active site structure and antigen binding properties of idiotypically cross-real A;Reference number: A34903; MUD:90094387; PMID:2104617
(A;Accession: C34903
(A;Accession: C34903
(A;Accession: C34903)
(A;Accession: C34003)
(A;Access
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           permease [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: E90446
R;She, Q.; Singh, R.K.; Confalonieri, P.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chandong, I.; Jeffries, A.C.; Rozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, E abmitted to GenBank, April 2001
A;Pescription: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: E90446
       A;Molecule type: mRNA
A;Residues; 1-1502 <HIRA
A;Cross-treferences: UNIPROT:088269; EMBL:AB010466; NID:g3242457; PIDN:BAA28954.1; PID:g3
A;Experimental source: strain Sprague-Dawley; liver
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q97VB7; GB:AE006641; NID:g13816037; PIDN:AAK42828.1; GSPDB:G
C;Genetics:
A;Gene: SSO2718
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                                                                                                                                                                                                                                           Query Match 78.6%; Score 44; DB 2; Length 1502; Best Local Similarity 50.0%; Pred. No. 80; Matches 5; Conservative 4; Mismatches 1; Indels
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Pred. No. 34;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.8%;
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Best Local Similarity 50.00,
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963 QGYWLSLWAD 972
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A;Molecule type: DNA
A;Residues: 1-419 <KUR>
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Best Local Similarity
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C.Species: Pyrococcus abyssi
C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C.Accesaion: C75176
R.Janonymous, Genoscope
Rubmitted to the EMBL Data Library, July 1999
A.Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struct A.Reference number: A75001
A.Accession: C75176
A.Accession: C7517730; PIDN:CAB49499(A.Accession: C75174730; PIDN:CAB49499(A.Accession: C75174730; PIDN:CAB49499(A.Accession: C75174730; PIDN:CAB494940(A.Accession: C75174730; PIDN:CAB494940(A.Accession: C751747480; PIDN:CAB49494(A.Accession: C751747480; PIDN:CAB49494(A.Accession: C751747480; PIDN:CAB49494(A.Accession: C751747480; PIDN:CAB49494(A.Accession: C75174480; PIDN:CAB49494(A.Accession: C75174480; PIDN:CAB49494(A.Accession: C75174480; PIDN:CAB49494(A.Accession: C75174480; PIDN:CAB49494(A.Accession: C75174480; PIDN:CA
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-475 <ZUN>
A;Residues: 1-475 <ZUN>
A;Cross-references: UNIPROT:053092; EMBL:AJ001330; NID:g2764610; PIDN:CAA04686.1; PID:g2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Zuniga, M.; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Martinez, J. Bacteriol. 180, 4154-4159, 1998
A;Title: Structural and functional analysis of the gene cluster encoding the enzymes of A;Reference number: Z23141; MUID:98361904; PMID:9696763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T50103 '''r
probable oxidoreductase [imported] - fission yeast (Schizosaccharomyces pombe)
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C;Species: Lactobacillus sakei
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T46745
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Cispecies: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
Cispecession: TS0103
Riseger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 2000
                                                                                                                                                                                                                                                                                                                antiporter (napa-2) PAB0390 - Pyrococcus abyssi (strain Orsay)
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Pred. No. 96;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: napA-2; PAB0390
C;Superfamily: Aquifex aeolicus Na+/H+-exchanging protein napA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.4%; Score 40; DB 2; Length 475; 62.5%; Pred. No. 1.1e+02;
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50.0%;
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Best Local Similarity 50.0
Matches 5; Conservative
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93 WGYWLSAW 100
                                                    :||| |||
392 EGYWDTIW 399
1 XGYWLTIW 8
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Matches 5; Conserv
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A;Residues: Lype: DNA
A;Residues: 1-508 ckUR>
A;Residues: 1-508 ckUR>
A;Cross-references: UNIPROT: 0930N2; GB: AE006469; PIDN: AAK64821.1; PID: g14523232; GSPDB: GA;Cross-references: UNIPROT: 0930N2; GB: AE006469; PIDN: AAK64821.1; PID: g14523232; GSPDB: GA;Cross-references: UNIPROT: 0930N2; GB: AE006469; P:; Barloy-Hubler, R:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, R:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Rederspiel, N.A.; Fisher, R.F.; Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; V. Lelaure, W. L. Jones, T. A. Long, R.W.; Long, R.W.; Lelaure, C. Lela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arginine/ornitine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL146
C,Species: Lactococcus lactis subsp. lactis
C,Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: C86879
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A;Cross-references: UNIPROT:Q9CE15; GB:AE005176; PID:g12725084; PIDN:AAK06133.1; GSPDB:G
A;Experimental source: strain IL1403
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C; Saccession: C52282
R; Barnett, M.J.; Fisher, R.P.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Nall, Acad. Sci. U.S.A. 98, 9833-9888, 2001
A; Title: Nucleotide sequence and predicted functions of the entire Sinochizobium melilot A; Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: C66879
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A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Weils, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
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                                                    Length 376;
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Pred. No. 78;
3; Mismatches 2; Indels
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                                                                                                                                          2; Indels
                                          Score 41; DB 2;
Pred. No. 60;
2; Mismatches
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C,Superfamily: L-lysine transport protein
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50.0%;
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ilarity 60.0%;
Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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A; Status: preliminary
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Cispecies: Alcaligenes eutrophus
Cispecies: Alcaligenes eutrophus
Cipate: 23-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 09-Jul-2004
Cipate: 23-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 09-Jul-2004
Cipatession: A33330
Rives, D.H.; Nies, A.; Chu, L.; Silver, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 7351-7355, 1989
A;Title: Expression and nucleotide sequence of a plasmid-determined divalent cation effluaremence number: A33330, MUID:90017477; PMID:2678100
A;Accession: A33830
A;Accession: A33830
A;Accession: A33830
A;Residues: 1-1063 *NIEs
A;Cross-references: UNIPROT:P13511; GB:M26073
C;Superfamily: cation efflux system membrane protein czcA
C;Keywords: transmembrane protein
                                                                                                        cation efflux system membrane protein czcA - Alcaligenes eutrophus
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nes 6; Conservative
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861 AGYWMT-WGG 869
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A;Reference number: Z25038
A;Accession: T50103
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residus: 1-583 <SEE>
A;Cross-references: UNIPROT:Q9US28; EMBL:AL136499; PIDN:CAB66164.1; GSPDB:GN00066; SPDB:A;Cross-references: strain 972h(-); cosmid c1783
C;Genetics:
A;Genetics: A;Genetics: A;Genetics: 1
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C;Species: Homo sapiens (man)
C;Dacession: S71847
R;Cullen, P.J.
Submitted to the EMBL Data Library, July 1995
A;Reference number: S71847
A;Accession: S71847
A;Accession: S71847
A;Status: preliminary
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A,Residues: 1-829 <CUL>
A,Residues: 1-829 <CUL>
A,Cross-references: EBBL:X89399; NID:g963051; PID:g963052
F,328-539/Domain: ras-specific GAP catalytic domain homology <GAP>
F;571-670/Domain: pleckstrin repeat homology <PLK>
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A;Residues: 1-829 <CUL>
A;Cross-references: EMBL:X89399
F;328-539/Domain: ras-specific GAP catalytic domain homology <CAP>
F;571-670/Domain: pleckstrin repeat homology <PLK>
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Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 2;
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688 SGHWLCCWGA 697
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243 GGRWPTIWGE 252
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688 SGHWLCCWGA 697
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Q775c7 bordetella
Aar97683 bordetell
Q8yx40 anabaena sp
Q8zus8 pyrobaculum
Q7nsj2 chromobacte
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Caf23898 parachlam
Q92zt6 rhizobium m
Q8h2n7 oryza sativ
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Aas08923 lactobaci
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                                               ; Search time 121.6 Seconds (without alignments) 47.317 Million cell updates/sec
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                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29kgv3
     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                              1825181 seqs, 575374646 residues
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AAS08923
06MC01
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003Z85
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Maximum Match 100%
Listing first 45 summaries
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Q8ZUS8
Q7NSJ2
Q9KGV3
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length DB
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093na rhizobium m
098574 lactococcus
082a22 streptomyce
07quc2 giardia lam
06m566 corynebacte
Caf21531 corynebac
08ed7 shewanella
09ex20 oryze sativ
09x160 pyrococcus
08v160 pyrococcus
  bradyrhizob
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EMBL, AE017203, AAS08923.1; -.. EMBL, AE017203, AAS08923.1; -.. InterPro; IPR004254; HlylII.
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
NCBL_TaxID=33959;
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
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Last annotation update)
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Pred. No. 54;
4; Mismatches
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Q9V160
Q8U016
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Q8NQB6
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TIGRFAMS; TIGR01065; hlyIII; 1.
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
Hemolysin-11ke protein.
OrderedLocusNames=LJ1101;
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02-MAR-2004 (TrEMBLrel. 27
02-MAR-2004 (TrEMBLrel. 27
^^-MAR-2004 (TrEMBLrel. 27
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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171 TGFWLLVWGG 180
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=33959;
 STRAIN=NCC 533;
PubMed=14966310;
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Gaps

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RESULT 3

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RA Barloy-Hubler F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,
Ra Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,
Ra Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P.,
RA Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
RA Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,
RA Harandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,
RA Man M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
RA Masuy D., Palm C., Peck M.C., Pohl T.M., Portecelle D., Purnelle B.,
Ramperger U., Surzycki R., Thebault P., Vandenbol M.,
Rondocter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
"The composite genome of the legume symbiont Sinorhizobium meliloti.";
Science 293168-672(2001).
RENBL, AE007228, AAK650211; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE=2136509; PubMed=11481432;
Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barnoy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
"Nuclectide sequence and predicted functions of the entire
Sinorhizobium meliloti psymA megaplasmid.";
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888 (2001).
an amoeba symbiont and its use for reconstructing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:0016021; C:integral to membrane; IEA.
GO:0006279; F:amino acid-polyamine transporter activity; IEA.
GO:0006865; P:amino acid transport; IEA.
GO:0006810; P:transport; IEA.
                                                                                                                              Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U. Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D., Rattei T., Mewes H., Wagner M.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium. NCBI TaxID=382;
                                                                                                                                                                                                                                                                                                          Score 44; DB 2; Length 284; Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                          1; Indels
  "Genome sequence of an amoeba symbiont and its use for r
the evolutionary history of chlamydiae.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                 284 AA; 33607 MW; 569E29F0D7F6AECA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 19, Last sequence update) (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          441 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OrderedLocusNames=RA0363; ORFNames=SMa0684; Rhizobium meliloti (Sinorhizobium meliloti)
                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
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InterPro; IPR004841; Permease_region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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MEDLINE=21368234; PubMed=11474104;
                                                                                                                                                                                                                      EMBL; BX908798; CAF23898.1; -.
                                                                                                                                                                                                                                                                                                            78.6%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probable transport protein.
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nes 5; Conservative
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271 QAYWLSLWGI 280
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                                                                                                                                                                                                                                             Hypothetical protein.
                                                                                        SEQUENCE FROM N.A. STRAIN=UWE25;
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX908798; CAF23898.1; -.
Hypothetical protein.
SEQUENCE 284 AA; 33607 MW; 569E29F0D7F6AECA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
Bacteria, Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
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Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
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                                                               Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C., Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann B., Barrangou R. Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.; "The genome sequence of the probiotic intestinal bacterium Lactobacillus johnsonii NCC 533."; Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004). EMBL; AR01203; AAS0823.1; - 101:2512-2517(2004).
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Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,
Rattei T., Mewes H.-W., Magner M.;
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Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,
Rattei T., Mewes H., Wagner M.;
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4; Mismatches
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Pred. No. 5
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les 5; Conservative
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Best Local Similarity
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                                                 PubMed=14966310;
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CAF23898;
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CAF23898
CAF23898
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DD CAF2
DT 14-A
DD 14-A
DE Hypo
GN PC111
COX NCB1
RN F11
RN SEQU
RC STRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeee, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name-Abcc6; Synonyms=Mrp6;
Nubs musculus (Mouse).
Eukaryota; Metaxoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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SEQUENCE FROM N.A.
STRAIN=ddY; TISSUBELiver;
STRAIN=ddY; TISSUBELiver;
Morikawa A., Suzuki H., Hirohashi T., Sugiyama Y.;
Morikawa A., Suzuki H., Hirohashi T., Sugiyama Y.;
Morikawa A., Suzuki H., Hirohashi T., Sugiyama Y.;
"Mus musculus mRNA for multidrug resistance-associated protein 6
"Mus musculus mRNA for multidrug resistance-associated protein 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ol-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Multidrug resistance-associated protein 6 (ATP-binding cassette, family C, member 6).
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                               78.6%; Score 44; DB 2; Length 441; 50.0%; Pred. No. 1.4e+02; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 2; Length 733;
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Sasaki T., Matayose Y.; Sasaki T., Matsumoto T., Katayose Y.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AP005486; BAC16197.1; -.
Pfam; PF00324; AA_permease; 1.
Complete proteome; Plasmid; Transmembrane; Transport.
SEQUENCE 441 AA; 46277 MW; B6FSC9EC96011AD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro, 198007658; DUP594.
Pfam, PF04578; DUP594; 1.
Hypothetical protein.
SEQUENCE 733 AA; 82939 MW; E95884DADIDC2AC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                    01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
101-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein OJ1138_B05.118.
                                                                                                                                                                                                                                                                                                                 733 AA
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                                                                             Query Match
Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                                                                                                 1 XGYWLTIWGX 10
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MRP6 MOUSE
AC 098187 M
AC 098187 M
AC 098187 M
DT 01-0CT
DT 01-0CT
DE family
GN Name=1,4
GN Name=1,4
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RP SEQUEN
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Q8H2N7
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Altschul F. P., Collins F. S., Wagner L., Shenmen C. M., Schuler G. D., Altschul F. P., Zeeberg B., Buerow K. H., Schaefer C. F., Bhat N. K., Hopkins R. F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A. A., Rubin G. M., Heng L., Stapleton M., Soares M. B., Toshiyuki S., Carninci P., Scheetz T. E., Bromstein M. J. Usdin T. B., Toshiyuki S., Carninci P., Prange C., A. Raha S. S., Loquellano N. A., Peters G. J., Abramson R. D., Mullahy S. J., Richards S., Worley K. C., Hale S., Garcia A. M., Gay L. J., Hulyk S. W., A. Hilalon D. K., Muzny D. M., Sodergren B. J., Lu X., Gibbs R. A., Fabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A. C., Shevchenko Y., Bouffard G. G., Antiquez A.C., Grimwood J., Schmutz J., Myers R. M., Schein J. B., Jones S. J., Marra M. A., Schein J. B., Jones S. J., Marra M. A., Schein J. B., Jones S. J., Marra M. A., Schein J. B., Jones S. J. M., Marra M. A., Schein J. B., Jones S. J. M., Marra M. A., Schein J. B., Jones S. J. M., Marra M. A., Schein J. B., Jones S. J. M., Marra M. A., Schein J. B., Jones S. J. M., Marra M. A., Schein J. B., Jones S. J. M., Marra M. A., Schein J. B., Jones S. J. M., Marra M. A., Schein J. B., Jones S. J. M., Marra M. A., Schein J. B., Jones S. J. M., Marra M. A., Schein Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (er) AfCS-Nature Molecule Pages (2004).

-!- FUNCTION: May participate directly in the active transport of drugs into subcellular organelles or influence drug distribution indirectly (By similarity).

-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

-!- SIMILARITY: Belongs to the ABC transporter family. MRP subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SMUCL...

TIGREAMS; TIGRO0957; MARE T. 2. A PROSITE; PSS00299; ABC_TMIP: 2. A PROSITE; PSS0093; ABC_TRANSPORTER 1; 1.

R PROSITE; PSS0093; ABC_TRANSPORTER 2; 2. A PROSITE; PSS0093; ABC_TRANSPORTER 2; 2. A PROSITE; PSS0093; ABC_TRANSPORTER 2; 2. A PROMAIN 37 Extracellular (By similarity).

FT TRANSMEM 38 (Cycoplasmic (By similarity).

FT TRANSMEM 59 78 Cycoplasmic (By similarity).

FT TRANSMEM 79 99 2 (By similarity).

FT TRANSMEM 79 99 2 (By similarity).

TOWAIN 79 99 2 (By similarity).
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Cytoplasmic (By similarity).
Gytoplasmic (By similarity).
Extracellular (By similarity).
5 (By similarity).
6 (By similarity).
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7 (By similarity).
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Extracellular (By Bimilarity).
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InterPro; IPR00140; ABC_TM_transpt.
InterPro; IPR001439; ABC_transporter.
InterPro; IPR005439; ABC_transporter.
Pfam; PF00064; ABC_membrane; 2.
Probom; PF000006; ABC_transporter; I.
SMART; SM00382; AAA; 2.
TIGREAMS; TIGR00957; MRP_assoc_pro; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences."
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MGD; MGI:1351634; Abcc6
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Pfami PF00664; ABC membrane; 2.
Pfam; PF00005; ABC tran; 2.
Prodom, PD000066; ABC transporter; 1.
SMART; SM00382; AAA; 2.
TIGRFAMS; TIGR00957; MRP_assoc_pro; 1.
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InterPro; IPR001140, ABC_TM transpt.
InterPro; IPR003499; ABC_transporter.
InterPro; IPR005292; MRP_assoc.
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EMBL; U73038; AAD12747.1; -.
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30-MAY.-2000 (Rel. 39, Last sequence update)
30-MAY.-2000 (Rel. 45, Last annotation update)
Multidrug resistance-associated protein 6 (ATP-binding cassette, sub-family C, member 6) (MRP-like protein-1) (MLP-1).
Name-Abcc6; Synonyms-Mrp6, Mlp1;
Rattus norvegicus (Rat).
Bukaryosa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TAXID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         liver.";
Mol. Pharmacol. 57:634-641(2000).
-!- FUNCTION: May participate directly in the active transport of drugs into subcellular organelles or influence drug distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
A - V (in Ref. 2).
I -> T (in Ref. 2).
H -> Q (in Ref. 2).
L -> V (in Ref. 2).
L -> V (in Ref. 2).
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MEDLINE-98279126; PubMed-9614210;
Hirohashi I., Suzuki H., Ito K., Ogawa K., Kume K., Shimizu T.,
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                                                                          11 (By similarity).

Cytoplasmic (By similarity).

Cytoplasmic (By similarity).

Extracellular (By similarity).

13 (By similarity).

Cytoplasmic (By similarity).

14 (By similarity).

Extracellular (By similarity).

15 (By similarity).

Extracellular (By similarity).
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17 (By similarity).
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ABC transporter 1.
ARC transporter 2.
ATP (Potential).
ATP (Potential).
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               Cytoplasmic (By similarity).
10 (By similarity).
Extracellular (By similarity).
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16 (By similarity).
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4; Mismatches 1;
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STRAIN=Sprague-Dawley; TISSUE=Liver;
MEDLINE=20159081; PubMed=10692506;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                         -1- SIMILARITY: Belongs to the ABC transporter family. MRP subfamily.
indirectly (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- TISSUB SPECIFICITY: High in liver and lower in duodenum and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1197 Extracellular (By similarity).
1218 17 (By similarity).
1502 Cytoplasmic (By similarity).
1503 ABC transporter 1.
1498 ABC transporter 2.
1668 ATP (Potential).
1305 ATP (Potential).
1305 ATP (Potential).
2 N-linked (GlonAc. . .) (Potential).
2 A3; 164995 MW; 539901B674A74A28 CRC64;
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R PROSITE; PSSO021; ABC_TRANSPORTER 1; 2.
R PROSITE; PSSO021; ABC_TRANSPORTER 2; 2.
M ATP-binding; Glycoprotein; Repeat; Transmembrane; Transport.
T DOMAIN 3 STA Extracellular (By similarity).
T TRANSMEM 39 78 Cytoplasmic (By similarity).
T TRANSMEM 100 104 Extracellular (By similarity).
FT TOOMAIN 105 125 3 (By similarity).
FT TRANSMEM 115 125 3 (By similarity).
FT TRANSMEM 115 125 3 (By similarity).
FT TRANSMEM 126 127 Cytoplasmic (By similarity).
FT TRANSMEM 138 125 173 Extracellular (By similarity).
FT TRANSMEM 195 30 Cytoplasmic (By similarity).
FT TRANSMEM 195 30 Cytoplasmic (By similarity).
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(Yopklasmic (By similarity).
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Extracellular (By similarity).
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MEDLINE-21988190; PubMed=11880368; DOI=10.1074/jbc.M110918200;
MIDLINE-21988190; PubMed=11880368; DOI=10.1074/jbc.M110918200;
Ilias Naradi B., Seidl T.L., Le Saux O., Sinko B., Boyd C.D.,
Sarkadi B., Varadi A.;
"Loss of ATP-dependent transport activity in pseudoxanthoma elasticum-
associated mutants of human ABCC6 (MRP6).";
J. Biol. Chem. 277:16860-16867(2002).
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=99425270; PubMed=10493829;
Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,
Loftus B.J., Mix U.-J., Sneddon V.B., Kantsead M., Cronin L.,
Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
Bichler E.B., Harris P.C., Venter J.C., Adams M.D.;
"Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";
Genomics 60:295-308(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Uitto J., Pulkkinen L., Ringpfeil F.;
"Modecular genetics of pseudoxanthoma elasticum: a metabolic disorder
at the environment-genome interface?";
Trends Mol. Med. 7:13-17(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION, AND CHARACTERIZATION OF VARIANTS PXE PHE-1298; ARG-1302 AND
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21321623; PubMed=11427982; DOI=10.1016/S1471-4914(00)01869-4;
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=99107222; PubMed=9892204;
KCOl M., van der Linden M., de Haas M., Baas F., Borst P.;
Expression of human MRP6, a homologue of the multidrug resistance protein gene MRP1, in tissues and cancer cells.";
Cancer Res. 59:175-182(1999).
                                                                                                                                                      O95255; P78420; O9UMZ7;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
31-OGT-2004 (Rel. 45, Last annotation update)
Multidrug resistance-associated protein 6 (ATP-binding cassette, femily C, member 6) (Anthracycline resistance-associated protein)
(Multi-specific organic anion tranporter-E) (MOAT-E).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Germain D.P., Perdu J., Remones V., Jeunemaitre X.; "Homozygosity for the R1268Q mutation in MRP6, the pseudoxanthoma
                                                                                                                                                                                                                                                                       Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99352020; PubMed=10424734;
Belinsky M.G., Kruh G.D.;
"MOAT-E (ARA) is a full-length MRP/cMOAT subfamily transporter
expressed in kidney and liver.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT GLN-1268.
MEDLINE=20374463; PubMed=10913334; DOI=10.1006/bbrc.2000.3101;
            Length 1502;
                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           elasticum gene, is not disease-causing.";
Biochem. Biophys. Res. Commun. 274:297-301(2000)
           Score 44; DB 1; I
Pred. No. 4.4e+02;
                                                                                                                                               PRT; 1503 AA
                                   4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVIEW, AND VARIANT PXE PRO-455.
           78.6%;
50.0%;
Query Match
Best Local Similarity 50..

Best S; Conservative
                                                                                                                                                 STANDARD;
                                                                                  963 QGYWLSLWAD 972
                                                            1 XGYWLTIWGX 10
                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                 HUMAN
                                                                                                                        RESULT 9
MRP6_HUMAN
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TRP-1121; PRO-1138; GLN-1138; ASP-1203; PHE-1298; ILB-1301; ARG-1302; PRO-1303; GLN-1314; TRP-1314; SRR-1321; CYS-1339; HIS-1347; ASN-1361; AND TRR-1424, AND VARIANTS ASP-61; ARG-207; GLY-265; GLU-281; VAL-3161; LYS-497; ALA-641; GLN-632; HIS-953; CYS-1241 AND GLN-1268. MEDLINE=21426347; PubMed=11536079; Is Saux O., Beck K., Sachsinger C., Silvestri C., Treiber C., Goering H.H.H., Johnson E.W., De Paepe A., Pope F.M., Pope F.M., Pagquali-Ronchetti I., Bercovitch L., Terry S., Boyd C.D.; "A spectrum of ABCC6 mutations is responsible for pseudoxanthoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Hum. Genet. 46:699-705(2001).

-1- FUNCTION: May participate directly in the active transport of drugs into subcellular organelles or influence drug distribution indirectly. Transports glutathione conjugates as Leukotriene-c4. (LTC4) and N-ethylmaleimide S-glutathione (NEM-GS).

-1- SÜBCELULAR LOCATION: Integral membrane protein (By similarity).

-1- TISSUS SPECIFICITY: Expressed in kidney and liver. Very low expression in other tissues.

-1- DISEASE: Defects in ABCC6 are a cause of autosomal dominant pseudoxanthoma elasticum (AD-PXE) [MIM:177850]. PXE is a disorder characterized by calcification of elastic fibers in skin, arteries and retina that results in dermal lesions with associated laxity
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20408303; PubMed=10554200; Struk B., Cai L., Zaech S., Ji W., Chung J., Lumsden A., Stumm M., Struk B., Cai L., Kim C.-A., Ji W., Chung J., Lumsden A., Stumm M., Piguera L.E., Fuchs W., Munier F., Ramesar R., Hohl D., Richards R., Neldner K.H., Lindpaintner K.; Ramesar R., Hohl D., Richards R., Mutations of the gene encoding the transmembrane transporter protein J. Mol. Med. 78:282-286(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS PXE PRO-1114; GLN-1138 AND TRP-1314, AND VARIANT ALA-614.
MEDIJNE=20296630; PubMed=10835642; DOI=10.1038/76102;
Le Saux O., Urban Z., Tschuch C., Csiszar K., Bacchelli B.,
Quaglino D., Paequali-Ronchetti I., Pope F.M., Richards A., Terry S.,
Bercovitch L., de Paepe A., Boyd C.D.;
"Mutations in a gene encoding an ABC transporter cause pseudoxanthoma
MEDLINE=20514578; PubMed=11058917; DOI=10.1002/1098-1004(20011)15:55449::AID-HUMU24>3.0.CO;2-O; DOI=10.1002/1098-1004(20011)15:55449::AID-HUMU24>3.0.CO;2-O; CErmain D.P., Perdu J., Remones V., Manzoni K., Jeunemaitre X.; Identification of two polymorphisms (c189G>C; c190T>C) in exon 2 of the human MRRF gene (ARCG6) by screening of Pseudoxanthoma elasticum patients: possible sequence correction?";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20283940; PubMed=10811882; DOI=10.1073/pnas.100041297; Ringpfeil F., Lebwohl M.G., Christiano A.M., Ultto J.; "Pseudoxanthoma elasticum: mutattions in the MRP6 gene encoding transmembrane ATP-binding cassette (ABC) transporter."; Proc. Natl. Acad. Sci. U.S.A. 97:6001-6006(2000).
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                                                                                                                                                                                                                                                                                                                                                                                              VARIANT PXE CYS-1339, AND VARIANT GLN-632.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genet. 25:223-227(2000).
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964 RGYWLSLWAD 973
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                                     RESULT 10
Q82Z85
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                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005624; C:membrane fraction; TAS.
GO; GO:0005886; C:plaema membrane; TAS.
GO; GO:0005824; F:ATP binding; TAS.
GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; TAS.
GO; GO:0005215; F:transporter activity; TAS.
GO; GO:0042493; F:reansporter activity; TAS.
GO; GO:006810; P:reapport; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             R InterPro; IPR00353; AAA, ATraes.
R InterPro; IPR00343; AAA, ATraes.
R InterPro; IPR00343; ABC_TM transpt.
R InterPro; IPR00343; ABC_Tmansporter.
R InterPro; IPR00343; ABC_Tmansporter.
R Pfam; PF00066; ABC_Tman; 2.
R Pfam; PF00006; ABC_Tran; 2.
R Pfam; PR00006; ABC_Tran; 2.
R Pfam; PR00018; AAA; Z.
R Pfam; PR0018; AAA; Z.
R PROSITE; PS50229; ABC_TRANSPORTER_1; 2.
R PROSITE; PS50829; ABC_TRANSPORTER_1; 2.
R PROSITE; PS5083; ABC_TRANSPORTER_2; 2.
R PROSITE; PS5083; ABC_TRANSPORTER_2; 2.
R PROSITE; PS50829; ABC_TRANSPORTER_2; 2.
R PROSITE; PS50829; ABC_TRANSPORTER_2; 2.
R Transmembrane; Transport; Vision.
                                                   SIMILARITY: Belongs to the ABC transporter family. MRP subfamily. CAUTION: Ref.2 sequence differs from that shown due to erroneous
                                                                            gene model prediction.
DATABASE: NAME=Mutations of the ABCC6 gene;
NOTE=Retina International's Scientific Newsletter;
WWW="http://www.retina-international.com/sci-news/abcc6mut.htm"
           hemorrhages leading to macular degeneration.
DISEASE: Defects in ABCC6 are a cause of autosomal recessive
pseudoxanthoma elasticum (AR-PXE) [MIM:264800].
loss of elasticity, arterial insufficiency and retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (By similarity).
Cytoplasmic (By similarity).
2 (By similarity).
Extracellular (By similarity).
3 (By similarity).
Cytoplasmic (By similarity).
4 (By similarity).
Extracellular (By similarity).
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Pred. No. 4.4e+02;
4; Mismatches 1; Indels
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Cytoplasmic (By similarity).
6 (By similarity).

Extracellular (By similarity).
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                                                                                                                                                                                                                                                         EMBL; AF076622; AAC79696.1; -.
EMBL; U91318; AAC15785.1; ALT_SEQ.
EMBL; AF168791; AAD51293.1; -.
HSSP; P08716; IMT0.
Genew; HGNC:57; ABCC6.
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450
471
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Best Local Similarity
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MEDLINE-22550857; PubMed=12663927; DOI=10.1126/science.1080613;
Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Ssehadri R.,
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barbay S., Blanchin S., Backerich J.M., Beyne B., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Barpons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerreet A., Kosuul R., Leaur I., Ma L., Muller H., Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.P., Straub M.L., Suleau A., Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B., Seniou-Meyer M., Zivanovic I., Bolotin-Pukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
                                                                                                                                                                              Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Ol-OCT-2004 (TrEMBLrel. 28, Last sequence update)
Ol-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to sp|P38071 Saccharomyces cerevisiae YBR026c.
ORFNames=YALIC19624;
Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Role of mobile DNA in the evolution of vancomycin-resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.8%; Score 43; DB 2; Length 266; 50.0%; Pred. No. 1.3e+02; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome; Hypothetical protein.
SEQUENCE 266 AA; 28291 MW; CD6E72C4DF555A36 CRC64;
                                                                            Last sequence update)
Last annotation update)
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                                                      Created)
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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 299:2071-2074(2003).
                                                 01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, Hypothetical protein.
                                                                                                                                                     OrderedLocusNames=EF3185;
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Matches 5: Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterococcus faecalis.";
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202 AGTWITLWGQ 211
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PERGUREE FROM N.A.

SEQUENCE FROM N.A.

STAIN=21332296; PubMed=11427726;

KREDLINE=21332296; PubMed=1142726;

KREDLINE=21332296; PubMed=1142726;

KREDLINE=21332296; PubMed=1142726;

KREDLINE=21332296;

KREDLINE=213323296;

KREDLINE=21332296;

KREDLINE=21332296;

KREDLINE=213323296;

KREDLINE=21332296;

KREDLINE=2
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"Ten families of variant genes encoded in subtelomeric regions of
multiple chromosomes of Plasmodium chabaudi, a malaria species that
undergoes antigenic variation in the laboratory mouse.";
Mol. Microbiol. 48:1209-1223 (2003).
EMBL, AN149028; AA066132.1;
SEQUENCE 1052 AA, 110704 MW; D6C5B3B3247C23B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium chabaudi chabaudi.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
76.8%; Score 43; DB 2; Length 1052;
Best Local Similarity 50.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.8%; Score 43; DB 2; Length 415
50.0%; Pred. No. 1.9e+02;
ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6DB6AB6B5C6DA267 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-07T-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBTGH2;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR00714; MFS.
InterPro; IPR005828; Sub.transporter.
Pfam; PF00083; Sugar tr; 1.
PROSITE; PS50850; MFS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1052 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1308 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=AS;
MEDLINE=22672904; PubMed=12787350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419 AA; 46499 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|:| |:||:
364 IGFWETLWGI 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      656 SGYWSNLWGT 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 XGYWLTIWGX 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 XGYWLTIWGX 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORFNames=PC10107c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=31271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7YZ84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
Q7YZ84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OBTEH2
ID OE
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DT 01
                  ACCOUNT REPORT OF THE REPORT O
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MEDLINE=20479972; PubMed=11029001;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapa
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Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Thermoplasmataceae, Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 50.0%; Pred. No. 1.9e+02; 5; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.8%; Score 43; DB 2; Length 376
60.0%; Pred. No. 1.8e+02;
cive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                             Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382129; CAG82338.1; -.
SEQUENCE 376 AA; 41206 MW; E085FF7C32379DCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      413 AA; 45192 MW; 307093BC358063D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 407:508-513 (2000).

EMBL; AL445065; CAC1830.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0005215; F:transporter activity; IEA.

GO; GO:0006810; P:transport; IEA.

InterPro; IPR007114; MFS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               413 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transport protein related protein.
                                                             'Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OrderedLocusNames=SSO2718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60..
Local Similarity 60..
Conservative
              Wincker P., Souciet J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OrderedLocusNames=Ta0692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50850; MFS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 KGYWLTRWAD 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|:| |:||:
353 IGFWETLWGI 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 XGYWLTIWGX 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 XGYWLTIWGX 10
                                                                                                   Nature 430:35-44(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                       (2)
SEQUENCE FROM N.A.
STRAIN=CLIB99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=2287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete p
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09HKA9
1D 099HKA
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CC Ther
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CC Arch
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Matches
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76.8%; Score 43; DB 2; Length 1308; 75.0%; Pred. No. 5.5e+02; ive 1; Mismatches 1; Indels
             Dictyostelium discoideum (Slime mold).
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ABC transporter ABCC.7.
Name=abcC7;
                                                                                                                                                     Query Match
Best Local Similarity 75.0%
                                   SEQUENCE FROM N.A.
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Search completed: January 3, 2005, 16:32:30 Job time : 122.6 secs

|||||| : 764 YWLTIWSD 771 3 YWLTIWGX 10

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Gaps

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2005
         Copyright
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- protein search, using sw model OM protein

Run on:

January 3, 2005, 16:33:55 ; Search time 147 Seconds (without alignments) 24.403 Million cell updates/sec

US-10-046-922-34 56

1 XGYWLTIWGX 10 score: Sequence: BLOSUM62DX 3 Gapext 0.5 Scoring table:

2002273 segs, 358729299 residues Searched:

444336 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB-seq_length: 10

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_23Sep04:* Database

geneseqp1990s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003bs:*geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

uo	VEGFR-3 b	VEGFR-3 b	Labaditin	Somatosta	Backbone	VEGFR-3 b	Human com	Antigenic	HLA bindi	HLA bindi	HLA bindi	Rhesus D	Rhesus D	HIV A11 m	HIV A03 B		HIV A03 m	HIV A03 m	HIV A02 8	HIV A03 8	HIV B27 8	HIV All m	Cyclic an	Anti-micr	Excluded	
Description	Abp53931	Abp53932	Aar14709	Aay76794	Abp53418	Abp53933	Aag95260	Aaw97529	Aau02369	Aau02282	Adn64476	Aab99759	Aab99758	Abp22594	Abp14287	Abp18686	Abp20292	Abp19992	Abp12050	Abp14288	Abp16999	Abp22402	Adh62029	Adp67844	Adg28067	
ID	ABP53931	ABP53932	AAR14709	AAY76794	ABP53418	ABP53933	AAG95260	AAW97529	AAU02369	AAU02282	ADN64476	AAB99759	AAB99758	ABP22594	ABP14287	ABP18686	ABP20292	ABP19992	ABP12050	ABP14288	ABP16999	ABP22402	ADH62029	ADP67844	ADQ28067	
DB	r.	Ŋ	7	m	S	'n	4	~	4	4	œ	4	4	4	4	4	4	4	4	4	4	4	æ	8	ω	
% Query Match Length	10	10	10	7	7	6	10	8	O	O	σ	10	10	œ	œ	œ	œ	œ	8	80	80	80	æ	80	60	
& Query Match	100.0	100.0	58.0	57.1	57.1	57.1	57.1			55.4	55.4	55.4	55.4	53.6	53.6	53.6	53.6	•		۳.	53.6	53.6	٠	53.6	53.6	
Score	26	26	32.5	32	32	32	32	31	31	31	31	31	31	30	30	30	30	30	30	30	30	30	30	30	30	
Result No.	п	7	e	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	

HIVO	ADP15275 HIV A24 B Abp15275 HIV A24 B
9 2 AAR37115 9 2 AAR37113 9 2 AAR737113 9 2 AAR73359 9 2 AAR7338 9 3 AAY74745 9 4 AAR72296 9 4 AAR72295 9 4 AAR72953 9 4 ABP25039	9 4 ABP15275
	30 53.6
0 7 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	* 4 * 0

ALIGNMENTS

Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor. VEGFR-3 binding peptide SEQ ID NO:34. ABP53931 standard; peptide; 10 AA (first entry) Homo sapiens. Synthetic. 09-JAN-2003 ABP53931; RESULT 1 ABP53931

'note= "any amino acid" Location/Qualifiers Misc-difference 10 Misc-difference

WO200257299-A2

/note= "any amino acid"

25-JUL-2002.

16-JAN-2002; 2002WO-IB000099.

(LUDW-) LUDWIG INST CANCER RES.

17-JAN-2001; 2001US-0262476P.

LICN) LICENTIA LTD.

Ξ,

Kubo

Koivunen E,

Alitalo K,

WPI; 2002-691521/74.

New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.

Claim 12; Page 80; 149pp; English.

The present invention describes an isolated peptide (I) that binds to and

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CGYWLTIWGC
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                            Jatropha multifida
                                                                            present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10 AA;
                                                                                                         Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-APR-1990;
                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
24-JAN-1992
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                                                                                                                                                                                                                                                      RESULT 3
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           have cytostatic, hepatotropic, antiinflammatory, hypotenalve, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for the call surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes an isolated peptide (1) that binds to and inhibits vascular endothelial growth factor receptor 3 (VGGRR-3). (1) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antiidabetic and valnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and terating disorders mediated by the activity of the cell surface receptor VBGFR-3 such as cancer, e.g. brain, lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
 inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth factor receptor 3 inhibitor; VEGFR-3;
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                                                                                                                                                                                                              100.0%; Score 56; DB 5; Length 10; 100.0%; Pred. No. 0.077; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           VEGFR-3 binding peptide SEQ ID NO:35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Page 80; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                ABP53932 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LUDW-) LUDWIG INST CANCER RES (LICN ) LICENTIA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JAN-2001; 2001US-0262476P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JAN-2002; 2002WO-IB000099.
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                                                                                                                                                                                                                                           10; Conservative
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                                                                                                                                                                                                                                                                   1 XGYWLTIWGX 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-691521/74.
                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                       Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200257299-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alitalo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                          ABP53932;
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liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 56; DB 5; Length 10; 80.0%; Pred. No. 0.077; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyclic; immunoglobulin; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR14709 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90US-00512796.
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                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 XGYWLTIWGX 10
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AGVW-TVWGT 9
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57.1%;

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Somatostatin analogue; therapy; cyclic peptide; autoimmune disease; endocrine disorder; cancer; diabetic-associated complication; diagnosis; gastrointestinal disorder; inflammatory disease; pancreatitis; atherosclerosis; restenosis; post-surgical pain; VIP secretion inhibitor; hormone-secreting tumour; hormone-dependent tumour; diarrhoea; vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.
                                                                                                                                                                        note= "D-form residue"
                                                                                                                                                                                                                                                                                               Gellerman G;
                                                                                                                                                        Location/Qualifiers
                                                                Somatostatin analogue peptide 3181.
                 AAY76794 standard; peptide; 7 AA.
                                                                                                                                                                                        /note= "Trp-NH2"
                                                                                                                                                                                                                                        99WO-IL000329
                                                                                                                                                                                                                                                        98US-00100360
98US-00203389
                                                (first entry)
                                                                                                                                                                                                                                                                                                Afargan MM,
                                                                                                                                                                                                                                                                                                                WPI; 2000-136888/12
                                                                                                                                                                                                                                                                               (PEPT-) PEPTOR LTD.
                                                                                                                                                                Misc-difference
                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                        15-JUN-1999;
                                                                                                                                                                                                                                                                02-DEC-1998;
                                                20-APR-2000
                                                                                                                                                                                                        WO9965508-A1
                                                                                                                                                                                                                        23-DEC-1999
                                                                                                                                                                                                                                                                                                Hornik V,
                                                                                                                                        Synthetic
                                AAY76794;
RESULT 4
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This sequence represents a somatostatin analogue of the invention. The invention relates to a backbone cyclised somatostatin analogue that has cone building unit contraining a nitrogen atom of the peptide backbone connected to a bridging group comprising an amide, thioether, thioester or disulphide. At least one building unit is connected from a second contraining the connected from a second building unit, side chain of or N-terminal amino acid residue. A composition containing the analogue may be used for preventing disorders out has cancers, autoinmune diseases, endocrine disorders, diabeticassociated complications, gastrointestinal disorders, inflammatory diseases, pancreatitis, atherosclerosis, restenosis and post-suggical pain. It may also be used for diagnosing cancer. The backbone cyclic analogues can be used for the treatment patients with hormone-secreting analogues can be used for the treatment patients with hormone-secreting and hormone-dependent tumours. They reduce diarrhoea through the inhibition of vasoactive intestinal peptide (VIP) secretion and by direct effect on intestinal secretion. Somatostatin analogues selective to type canders mellitus. They are useful for the prevention of atherosclerosis and restenosis. The analogues are metabolically stable, selective in their in-vivo activities and safe Cyclized somatostatin analogs for inhibiting growth hormone secretion from anterior pituitary and as antiproliferative agents for the treatment of tumors. Example 11; Page 61; 82pp; English.

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Sequence 7 AA;
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Query Match

57.1%; Score 32; DB 3; Length 7;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid residue. (I) has antiarteriosclerotic, immunosuppressive, cytostatic, antidiabetic, antiinflammatory and analgesic activities, and can be used as a somatostatin receptor ligand. (I) are useful in the treatment of atherosclerosis, autoimmune diseases, cancers, diabeticassociated complications, endocrine disorders, inflammation, gastrointestinal disorders, pancreatitis, post-surgical pain, and
                                                                                                                                                                                                                                                                                                                               Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic; somatotropin release inhibiting factor; somatostatin receptor subtype; synthesis; antiatreriosclerotic; immunosuppressive; cytostatic; cancer; antidiabetic; antiinflammatory; somatostatin receptor ligand; atherosclerosis; autoimmune disease; diabetic-associated complication; endocrine disorder; inflammation; gastrointestinal disorder; restenosis;
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New backbone cyclized somatostatin analogs are e.g. useful in the treatment of atherosclerosis, autoimmune diseases and cancers.
                                    ö
                                    Indels
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Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                               Backbone cyclised somatostatin analogue PTR 3181.
                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "D form residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                          pancreatitis, post-surgical pain.
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                                                                                                                                                                                          ABP53418 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                              19-NOV-2002 (first entry)
                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hornik V, Afargan MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AFAR/) AFARGAN M M. (GELL/) GELLERMAN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-681319/73.
                  Best Local Similarity
Matches 4; Conserv
                                                                    2 GYWLTIW 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HORN/) HORNIK V.
                                                                                                     1 GYWKVCW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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ABP53418
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Length 9;

Matches

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RESULT

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The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides interact with their relevant target proteins encoded in the human genome. They can be used as reagents in drug discovery and as lead ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A set of peptide ligands consisting of specific complementary peptides proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are drug
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; complementary peptide; ligand; drug discovery; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.1%; Score 32; DB 4; Length 10; 55.6%; Pred. No. 2.5e+02; ive 2; Mismatches 2; Indels
                                     Score 32; DB 5; 1
Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                             Human complementary peptide, SEQ ID NO: 1454.
                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Page 250; 646pp; English
                                                                                                                                                                                                                                                                       AAG95260 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW97529 standard; peptide; 8 AA.
                                       57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-DEC-2000; 2000WO-GB004776.
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                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        candidates or pro-drugs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                     Query Match
Best Local Similarity
                                                                                                                                                  SGYWWDIW
                                                                                                                       1 XGYWLTIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200142277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                          18-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roberts GW,
                                                                                                                                                                                                                                                                                                                 AAG95260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW97529;
                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, there is spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
restenosis. (I) can also be used in the diagnosis of cancer, by imaging the existence of metastases, it being labeled with a detectable probe. The present sequence represents a backbone cyclised somatostatin analogue from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
                                                                                                                                                                                                            ö
                                                                                                                                                                   Score 32; DB 5; Length 7; Pred. No. 1.7e+06; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEGFR-3 binding peptide SEQ ID NO:36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 14; Page 80; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 ABP53933 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LUDW-) LUDWIG INST CANCER RES (LICN ) LICENTIA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-2001; 2001US-0262476P.
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                                                                                                                                                                   57.1%;
57.1%;
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                                                                                                                                                                                                          4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-691521/74.
                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                    GYWLTIW 8
                                                                                                                                                                                                                                                                                             GYWKVCW
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                                                                                                                          Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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Homo

AAPPS3933
AAPPS39333
AAPPS3933
AAPPS

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Gaps

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Antigenic site of HN protein loop beta-4L23.

19-MAY-1999 (first entry)

present invention

Sequence 9 AA

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AAU02225-AAU02384 represent TADG-16 peptides which are tested for their binding affinity to the 8 haplotypes HLA A0201, HLA A0205, HLA A1, HLA A24, HLA B7, HLA B9, HLA B2702, and HLA B4603. Thour antigen derived gene-16 protein, TADG-16 (AAU0223), is a novel human extracellular serine protease. TADG-16 is expressed in normal ovaries and testes and in certain ovarian carcinomas. TADG-16 contains the conserved catalytic triad, His-Asp-Ser, and a signal secretion sequence characteristic of the serine protease family. An antisense oligonucleotide having a complementary sequence to the TADG-16 nucleic acid is useful for treating various cancers, including ovarian, breast, lung, colon and proteate. The TADG-16 nucleic acid is useful for treating are useful for the diagnosis of cancer. TADG-16 protein or its fragments are useful for vaccinating an individual against TADG-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU02225-AAU02284 represent TADG-16 peptides which are tested for their binding affinity to the 8 haplotypes HLA A0201, HLA A0205, HLA A1, HLA A24, HLA B7, HLA B7, HLA B7, TA B2702, and HLA B4403. Tumour antigen derived gene-16 protein, TADG-16 (AAU02223), is a novel human extracellular serine protease. TADG-16 is expressed in normal ovaries and testes and in certain ovarian carcinomas. TADG-16 contains the conserved catalytic triad, His-Asp-Ser, and a signal secretion sequence characteristic of the serine protease family. An antisense oligonucleotide having a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protease; tumour antigen derived gene-16; breast cancer; lung cancer; colon cancer;
      tumor antigen-derived gene-16 protein, useful for diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New tumor antigen-derived gene-16 protein, useful for diagnosis and treatment of ovarian, breast, lung, colon and prostate cancer.
                        treatment of ovarian, breast, lung, colon and prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.4%; Score 31; DB 4; Length 9; 57.1%; Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shigemasa K;
                                                                  Example 8; Page 55; 124pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU02282 standard; peptide; 9 AA.
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU02282;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
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                                                                                                                                                                                                                                                                                                                                                                                                          Isolated proteinaceous substance - comprising at least one virus epitope derived from an attachment protein of a paramyxovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuraminidase (HN) protein of the paramyxoviridae. The specification describes 3-D models identifying a proteinaceous substance comprising at least one virus epitope derived from the attachment protein, which corresponds to an antigenic site present on one of the loops of HN. The antigenic sites can be used to produce vaccines, to detect the viruses, and to select the immunodominant epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW97452-571 represent antigenic sites derived from the haemagglutinin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protease; tumour antigen derived gene-16; breast cancer; lung cancer; colon cancer;
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Antigenic site; haemagglutinin-neuraminidase; HN; paramyxoviridae; virus epitope; attachment protein; vaccine; immunodominant epitope
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                                                                                                                                                                                                                                                                             (DIER-) STICHTING INST DIERHOUDERIJ EN DIERGEZON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.4%; Score 31; DB 2; Le 100.0%; Pred. No. 1.7e+06; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shigemasa K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 48; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU02369 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                          Van Oirschot JT;
                                                                                                                                                                                           98WO-NL000390.
                                                                                                                                                                                                                                   97EP-00202100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TADG-16; ovarian carcinoma;
prostate cancer; HLA type.
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                       Langedijk JPM,
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                                                                Measles virus.
                                                                                                                                                                                                                                   08-JUL-1997;
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                                                                                                                                                                                           08-JUL-1998;
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complementary sequence to the TADG-16 nucleic acid is useful for treating various cancers, including ovarian, breast, lung, colon and prostate. The TADG-16 nucleic acid, TADG-16 protein and antibodies specific to TADG-16 are useful for the diagnosis of cancer. TADG-16 protein or its fragments are useful for vaccinating an individual against TADG-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New composition of peptides and nucleic acids capable of binding Major Histocompatibility Complex molecules, useful for diagnosing, preventing or treating viral infections or cancer, such as prostate cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; hepatotropic; virucide; antiinflammatory; anti-HIV; gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome; prostate specific antigen; prostate specific membrane antigen; hepatitis B virus antigen; malignant melanoma antigen; MAGE; Epstein Barr virus; cancer; prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to a novel composition comprising one or more
                                                                                                                                                                                                     ô
                                                                                                                                                               Length 9;
                                                                                                                                                               Score 31; DB 4; I Pred. No. 1.7e+06;
                                                                                                                                                                                                     2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sette A;
                                                                                                                                                                                                                                                                                                                                                                                 ADN64476 standard; peptide; 9 AA.
                                                                                                                                                           55.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-OCT-2002; 2002US-0416207P.
08-OCT-2002; 2002US-0417269P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLA binding peptide #1076
                                                                                                                                                                                                     4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chondyloma acuminatum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIM-) EPIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-347953/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hepatitis B or AIDS.
                                                                                                                                                                                                                                            WLTIWGX 10
                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                               1 WVTGWGY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004031211-A2
                                                                                                                          Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-APR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                                        ADN64476;
                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                 ADN64476
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The present sequence represents a peptide capable of binding Rhesus D antibodies (I). Also described in the present invention are: (1) a uncleic acid (II) encoding (II); (2) a vector (III) comprising one or more (III) operably linked to an expression control system; (3) a cell (IV) comprising (II) or (III); (4) preparing (I); (5) identifying (M1) comprising immunologic properties of Rhesus D protein recognising an antibody/antibody fragment recognising an epitope of Rhesus D protein to several panning rounds with a phage comprising subjecting an antibody/antibody fragment recognising an epitope of Rhesus D protein; and (6) peptide sequences which are minotopes which differ in their amino acid sequence from the amino acid sequences of Rhesus D protein; and (6) peptides (V) with immunological properties of Rhesus D protein epitopes obtained by (M1). (1) is used to cannifecture an agent for the diagnosis, therapy or prophylaxis of the chiseases associated with Rhesus D antigen, e.g. haemolytic disease of the manufacture of an affinity reagent for anti-Rhesus D antibodies purified or removed from body fluids or immunoglobulin preparations. Using (I) as an immunogen to raise anti-Rhesus D antibodies avoids using immunisation of with forcest perturbors the properties of the properties thereby avoiding the risk of transmission of
                                                                                                                                     ö
acuminatum. The composition is also be used for diagnosing such diseases. This sequence represents a peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel peptides capable of binding Rhesus D antibodies are used to manufacture an agent for the diagnosis, therapy or prophylaxis of diseases associated with Rhesus D antigen, e.g. hemolytic disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhesus D antibody binding peptide; Rhesus D; RhD; identification; anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy; prophylaxis; haemolytic disease of the newborn; HDN; ITP; idiopathic thrombocytopaenic purpura; immunoglobulin.
                                                                                                                                       ö
                                                                                                                                     Indels
                                                                                                  Length 9;
                                                                                                                                       ;
                                                                                                  Score 31; DB 8; Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                         Rhesus D antibody binding peptide SEQ ID NO:4.
                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   viral diseases like AIDS and hepatitis B
                                                                                                                                                                                                                                                                                                               AAB99759 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fisch I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 12; 19pp; English.
                                                                                                55.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99EP-00122858
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                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                         3, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ZLBB-) ZLB BIOPLASMA AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hofmann A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-383568/41.
                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                             ω
                                                                                                                                                                                                    4 WLTIW
                                                               Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP1106625-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HDN)
                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miescher S,
                                                                                                                                                                                                                                                                                                                                                    AAB99759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              newborn
                                                                                                                                       Matches
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Gaps

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Indels

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AAB99758 standard; peptide; 10 AA.
                                                                                                                                                                                            Claim 1; Page 12; 19pp; English.
               Conservative
                                                                                                                                                (ZLBB-) ZLB BIOPLASMA AG
                       GYWLTIWGX 10
                               GYWSAKWAV 9
                                                                                                                                                                WPI; 2001-383568/41.
           Local Similarity
                                                                                                                                                                                                                                                                                          Sequence 10 AA;
                                                                                                        Homo sapiens
                                                                                                                EP1106625-A1
                                                                                                                                17-NOV-1999;
                                                                                                                                        17-NOV-1999;
Sequence 10
                                                                    21-SEP-2001
                                                                                                                        13-JUN-2001.
                                                                                                                                                        Miescher S,
                                                           AAB99758;
       Query Match
            Best Loc
Matches
                                           RESULT 13
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human immunodeficiency virus-1 (HIV-1) group comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequences (ABL2347 to ABR25397). (1) has virucide activity and can be used in vaccines. (1) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccines compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunospenses to andigens, which the use of group-based vaccines An additional advantage of an group-based vaccine approach is the ability to combine selected groups. (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Livingston BD,
  Pred. No. 3.5e+02;
3; Mismatches 3;
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Grey HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 32; Page 332; 448pp; English
                                                                                                                                                                                                                                            ABP22594 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Southwood
Kubo RT,
                                                                                                                                                                                                                                                                                                                                                                                                                   HIV All motif env peptide #317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-OCT-2000; 2000WO-US027766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-00412863.
40.08;
                                                                                                                                                                                                                                                                                                                                                                (first entry)
  Best Local Similarity 40.0
Matches 4; Conservative
                                                                                                  : |: | |:
1 KGFWDREWGL 10
                                                                         1 XGYWLTIWGX 10
                                                                                                                                                                                                                                                                                                                                            (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EPIM-) EPIMMUNE INC.
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Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-354887/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200124810-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-OCT-1999;
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15-JUL-2002
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Baker DM,
                                                                                                                                                                                                                                                                                            ABP22594;
                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                                        ABP22594
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                                                                                                                      셤
                                                                                                                                                                                                                                                                        The present sequence represents a peptide capable of binding Rhesus D antibodies (1). Also described in the present invention are: (1) a nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more (II) operably linked to an expression control system; (3) a cell (IV) comprising (II) or (III); (4) preparing (I); (5) identifying (M1) comprising while this mannologic properties of Rhesus D protein epitopes of Comprising an antibody/antibody fragment recognising an epitope of Rhesus D protein to several panning rounds with a phage display library, and identifying immunogenic peptide sequences which are minotopes which differ in their amino acid sequences of Rhesus D protein, and (6) peptides (V) with immunological properties of Rhesus D protein epitopes obtained by (M1). (I) is used to manufacture an agent for the diagnosis, therapy or prophylaxis of manufacture of an affinity reagent for anti-Rhesus D antibodies purified or removed from body fluids or immunoglobulin preparations. Using (I) as an immunogen to raise anti-Rhesus D antibodies avoide using immunisation of viral diseases like ADS and hepatitis B
                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel peptides capable of binding Rhesus D antibodies are used to manufacture an agent for the diagnosis, therapy or prophylaxis of diseases associated with Rhesus D antigen, e.g. hemolytic disease of the newborn (HDN)
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhesus D antibody binding peptide; Rhesus D; RhD; identification; anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy; prophylaxis; haemolytic disease of the newborn; HDN; ITP; idiopathic thrombocytopaenic purpura; immunoglobulin.
                                                                                                  ö
                                                  Length 10;
                                               Score 31; DB 4; Length 10;
Pred. No. 3.5e+02;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhesus D antibody binding peptide SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hofmann A, Fisch I;
                                                  55.4%;
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Cheanut

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Gaps
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 Score 30; DB 4; Length 8; Pred. No. 1.7e+06; 2; Mismatches 0; Indels
  53.6%;
                           4; Conservative
Query Match
Best Local Similarity
Matches 4; Conserv
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55.4%; Score 31; DB 4; Length 10;

Query Match

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The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of the antigens. Purhermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP25412 represent peptide sequences used in the examplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chesnut R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Southwood S, Livingston BD, Kubo RT, Grey HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV A03 super motif env peptide #27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 32; Page 161; 448pp; English.
                                                                                                                                                                                                                                                             ABP14287 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus 1
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                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sette A, Sidney J,
Baker DM, Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-354887/37
LTIWGX 10
                                          ||:||:
LTVWGI 7
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15-JUL-2002
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                                                                                                                                                                                    RESULT 15
ABP14287
XX ABP14
XX ABP14287
DT 11-SE
DT 11-SE
DT 11-SE
DY NOCO
XX HUMAN
XX WO200
XX HUMAN
XX CEPIN

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Db 2 LTVWGI 7
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Search completed: January 3, 2005, 16:56:47 Job time: 149 secs

Query Match
Best Local Similarity 66.79
Matches 4; Conservative

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0; Gaps

53.6%; Score 30; DB 4; Length 8; 66.7%; Pred. No. 1.7e+06; ive 2; Mismatches 0; Indels

5 LTIWGX 10

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US-09-311-784A-348
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Sequence 14, Appl
Sequence 17, Appl
Sequence 1495, Ap
Sequence 1495, Ap
Sequence 1550, Ap
Sequence 157, Appl
Sequence 1587, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 1500, Ap
Sequence 1500, Appl
Sequence 1655, Appl
Sequence 1655, Appl
Sequence 1655, Appl
Sequence 1655, Appl
Sequence 2474, Appl
Sequence 2474, Appl
Sequence 27, Appli
Sequence 27, Appli
Sequence 2, Appli
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17.924 Million cell updates/sec
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/cgn2_6/ptodata/1/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/jaa/RCTUS_COMB.pep:*
/cgn2_6/ptodata/1/jaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-735-253-8

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US-09-125-641-3

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US-09-125-641-3

US-09-125-641-3

US-09-125-641-3

US-09-125-641-195

US-09-350-641C-1587

US-09-350-641C-1587

US-09-350-641C-1587

US-09-350-641C-1587

US-09-130-128

US-08-131-128

US-08-131-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                  - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62DXI;
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued Patents AA:*
                                                                                                                                                                                                                                                                                 US-10-046-922-34
56
                                                                                                                                                                                                                                                                                                                                             1 XGYWLTIWGX 10
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum_DB_seq_length: 10-
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                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INCORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Sette, Alesandro Gary G.
APPLICANT: Sette, Alesandro
APPLICANT: Sette, Alesandro
APPLICANT: Cette, Alesandro
APPLICANT: Lavingston, Brian
APPLICANT: Chenul, Robert W.
APPLICANT: Chenul, Robert W.
TITLE OF INVENTION: Expression Vectors for Stimulating an TITLE OF INVENTION: Expression Vectors for Stimulating an TITLE OF INVENTION: Immune Response and Methods of Using the FILE REFERENCE: 39963-2002.01
CURRENT APPLICATION NUMBER: US 60/085,751
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR PILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-08-735-253-8

Sequence 8, Application US/08735253

Sequence 8, Papplication US/08735253

Patent No. 5942491

GENERAL INFORMATION:
APPLICANT: Root-Bernstein, Robert S.

TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Arthritis
NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS: 19

ADDRESSEE: Dressler, Goldsmith, Milnamow & Katz, Ltd.

STREET: 180 N. Stetson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30; DB 4; Length 9; Pred. No. 3.8e+05; 2; Mismatches 0; Indels
       US-09-125-641-1

US-09-125-641-2

US-09-125-641-2

US-09-852-874A-5

US-08-882-876-13

US-08-98-526-13

US-08-98-526-13

US-08-208-86C-87

US-08-208-86C-87

US-08-704-744-89

US-08-704-744-89

US-08-200-793B-64

US-08-200-793B-64

US-08-290-793B-68

US-08-290-793B-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . OTHER INFORMATION: HIVI ENV 61 (peptide 25.0032)
US-09-311-784A-348
                                                                                                                                                                                                                                                                                                                                                                               Sequence 348, Application US/09311784A
Patent No. 6534482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTIWGX 10
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LTVWGI 9
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAY, Brian K
FRELINGER, Jeffrey A
HYDE-DERCHER, Robin P
TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING
COMPLEMENTARY COMBINATORIAL LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORPUTER: FORPY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
CORPEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,827A
FILING DATE: 30-Apr-1998
CILING DATE: 31-MAR-1998
APPLICATION NUMBER: US 09/050,359
FILING DATE: 31-MAR-1999
APPLICATION NUMBER: PCT/US97/19638
FILING DATE: 31-OCT-1997
APPLICATION NUMBER: US 08/740,671
FILING DATE: 31-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
                                                                                                                                                                    53.6%; Score 30; DB 2; Length 10; 37.5%; Pred. No. 1.5e+02; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.8%; Score 29; DB 4; ilarity 57.1%; Pred. No. 3.8e+05; Conservative 0; Mismatches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: FOWLKES=4C TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-09-069-827A-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 28,005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 94, Application US/09069827A Patent No. 6617114 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202) 628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (202) 737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FOWLKES, Dana M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 94: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                    3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                              3 YWLTIWGX 10
TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                              1 FWRFLWGS 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 YWLTIWG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-09-069-827A-94
                                                                                                             US-08-735-253-13
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Patent No. 5942491
GENERAL INFORMATION:
APPLICANT: ROOt-Bernstein, Robert S.
TITLE OF INVENTION: Methods and Compositions for Treating TITLE OF INVENTION: Archritis
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dressler, Goldsmith, Milnamow & Katz, Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: 10.5.A.

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,253
FILING DATE:
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30; DB 2; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: No. 5942491thrup, Thomas E.
REGISTRATION NUMBER: 33,268
REDESTRATION NUMBER: MIC3302P0010US
TELECOMMUNICATION INFORMATION:
TELEPAK: (312) 616-5460
TELEPAK: (312) 616-5460
TELEPAK: (3120 616-5460)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
ATTORNEY/AGENT INPORMATION:
NAME: No. 5942491thrup, Thomas E.
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: MIC3302P0010US
TELEPHONE: (312) 616-5400
TELEPHONE: (312) 616-5400
INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 N. Stetson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-735-253-8
                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 3; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 YWLTIWGX 10
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1 FWRFLWGS 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Chicago
STATE: Illinois
                                                      U.S.A.
                                                                                  60601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                        STATE: I1 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-08-735-253-13
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Gaps

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LOCATION: 1..2
OTHER INFORMATION: /label= Variant residues ·
OTHER INFORMATION: /note= "Phe is in the D conformation and is OTHER INFORMATION: linked to DTPA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.8%; Score 29; DB 4; Length 10;
80.0%; Pred. No. 2.1e+02;
tive 1; Mismatches 0; Indels
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ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURENT APPLICATION DATA:

PILING DATE: 22-APR-1996

CLASSIFICATION: 424

ATYCRNEY/AGENT INFORMATION:

NAME: No. 6241965nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 92,385-DD

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPRAX: 312-715-1000

TELEPRAX: 312-715-1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: MCBride, William
APPLICANT: MCBride, William
APPLICANT: Dean, Richard T.
TITLE OF INVENTION: Somatostatin Derivatives
TITLE OF INVENTION: And their Radiolabeled Products
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
                REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 4-900-9862/A/NFI/PCT
REFECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEFAX: (908) 522-6923
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acids
STRANBENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SBE: Banner & Witcoff, Ltd.
: 10 South Wacker Drive, Suite 3000
Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/08586670A Patent No. 6241965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: YES
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-09-125-641-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 XGYWL 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Chicago
STATE: IL
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
US-08-586-670A-17
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                                                                                                                                                                                                                                                                                 APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
APPLICANTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE OF INVENTION: PROPERTIES
FILE OF INVENTION NUMBER: US/09/315,304B
CURRENT PILING DATE: 1998-05-20
RIOR PILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FASESEQ for Windows Version 3.0
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Sequence 3, Application US/09125641

Batent No. 6610297

GENERAL INFORMATION:
APPLICANT: Stadier, Beda
TITLE OF INVENTION: Peptide Immunogens For Vaccination
STREET: Sed Morris 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6610297artis Corporation
STREET: 564 Morris Avenue
CITY: Summit Avenue
CITY: Summit COMPUTER READBLE FORM:
COMPUTER READBLE FORM:
MEDIUM TYPE: FORDS MS-DOS
SOFTWARE: DEADBLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OFFICIATION DATA: US-AU
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/09/125,641
FILING DATE: 28-FEB-1997
PRIOR APPLICATION NUMBER: US/09/125,641
FILING DATE: 21-AUG-1998
FILING DATE: 28-FEB-1997
PRIOR APPLICATION NUMBER: QB 9604412.8
FILING DATE: O1-MAR-1996
PRIOR APPLICATION NUMBER: QB 9604412.8
FILING DATE: O1-MAR-1996
PRIOR APPLICATION NUMBER: QB 9604412.8
FILING DATE: O1-MAR-1996
PRIOR APPLICATION NUMBER: QB 9604412.8
FILING DATE: 22-AUG-1996
PRIOR APPLICATION NUMBER: QB 9604412.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 29; DB 3; Length 8; Pred. No. 3.8e+05; 3; Mismatches 1; Indels
                                                                                                                          Sequence 1649, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 42.5
Matches 3; Conservative
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WNSLWGW 7
                                                                        RESULT 5
US-09-315-304B-1649
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ORGANISM: HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-315-304B-1649
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NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1495
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                                                                                                                                                Query Match
Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Conservative
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Best Local Similarity
Matches 3; Conserv
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WDSLWGW 7
                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                      ; TYPE: PRT
; ORGANISM: HIV-1
US-09-834-784-1495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: HIV-1
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US-09-315-304B-1587
                                                                                                                                                                                                                                                                                                                                         US-09-350-641C-1650
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                                                        LENGTH: 8
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                 NAME/KEY: Modified-site
LOCATION: 1..4
COTHER INFORMATION: /label= Variant residues
OTHER INFORMATION: /note= "The Phe is in the D conformation; Xaa
OTHER INFORMATION: is L-4-chlorophenylalanine; the TEP is in the
FRATURE:
                                                                                                                                                                                                         /note= "The carboxyl group of the C-terminal
Thr is reduced to an alcohol;
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                                                                                                                                                                                                                                                                                                                        1; Indels
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                                                                                                                                                                                                                                                                                   50.0%; Score 28; DB 3; Length 8; 66.7%; Pred. No. 3.8e+05; ive 1; Mismatches 1; Indels
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Sequence 1495, Application US/09834784

Setent No. 6562787

GENERAL INFORMATION:
APPLICANT: Barney, Selly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohmed
APPLICANT: Anwer, Mohmed
APPLICANT: Anwer, Mohmed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/082,279

PRIOR FILING DATE: 1998-05-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohmed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
FULE REPERENCE: 1872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1988-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 3.8e+05;
                                                                                                                                                  CTHER INFORMATION: /label= Variant residues
CTHER INFORMATION: /note= "The carboxyl grou
CTHER INFORMATION: Thr is reduced to an alray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1495, Application US/09082279B Patent No. 6288782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.0%;
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Conservative
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Best Local Similarity
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1 FGYWKT 6
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; ORGANISM: HIV-1
US-09-082-279B-1495
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US-09-834-784-1495
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APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRER 1999-50-60
PRIOR REPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/0115,304
PRIOR PELING DATE: 1998-05-20
PRIOR PELING DATE: 1998-05-20
SOFTWARE: PSELSEQ for Windows Version 3.0
SOFTWARE: PSELSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES
FILE REFERENCE: 7872-052
CURRENT FILING DATE: 1999-05-20
PRIOR PILING DATE: 1999-05-20
PRIOR PILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARRE: FastSEQ for Windows Version 3.0
                                                                 Gaps
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Score 28; DB 4; Length 8; Pred. No. 3.8e+05; 3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                  , Sequence 1650, Application US/09350641C; Patent No. 6656906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1587, Application US/09315304B Patent No. 6348568
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RESULT 14
US-09-620-091-28
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       FEATURE:
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APPLICANT: Lambert, D.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-067
CURRENT APPLICATION NUMBER: US/09/350,641C
CURRENT APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FREEKS FEEKS FEEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ding, S.
APPLICANT: Kang, M.
APPLICANT: Kang, M.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ADMINISTRATION OF PILE OF INVENTION: THERAPBUTIC REAGENTS
FILE REPERENCE: 7872-062
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Pred. No. 2.9e+02;
3; Mismatches 3; Indels
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Pred. No. 2.9e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION WUMBER: US/09/350,325
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 47
LENGTH: 10
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Sequence 1587, Application US/09350641C

PARENT NO. 6656906

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Meturka, G.

APPLICANT: Meturka, G.

APPLICANT: Lambert, D.
                                                                                                          FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-3048-1587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: enhancer peptide US-09-350-325-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 47, Application US/09350325
Patent No. 6541020
GENERAL INFORMATION:
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 33.3%;
Matches 3; Conservative
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 33.3%;
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         2 GYWLTIWGX 10
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LENGTH: 10
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US-09-350-325-47
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GENERAL INFORMATION:

APPLICANT: CHIRLA, STEVEN B.

APPLICANT: BALU, PALANI

APPLICANT: BALU, PALANI

APPLICANT: BILU, PALANI

APPLICANT: BIPLANI, SUNILA

APPLICANT: BIPLANI, SUNILA

APPLICANT: BIPLANI, SUNILA

TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY

TITLE OF INVENTION: STIMULATING PACTOR RECEPTOR (G-CSFR) AND ASSOCIATED

TITLE OF INVENTION: USES

TITLE OF INVENTION: USES

TITLE OF INVENTION: USES

TITLE OF INVENTION: USES

CURRENT APPLICATION UNDEER: US/09/620,091

CURRENT APPLICATION UNDEER: US/09/620,091

SOFTWARE: PALENTE OF SEQ ID NOS: 491

SEQ ID NO 28

LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide
US-09-620-091-28
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                                                                                   Length 10;
                                                                             Query Match 50.0%; Score 28; DB 4; Length 10; Best Local Similarity 33.3%; Pred. No. 2.9e+02; Matches 3; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%; Score 28; DB 4; Length 10;
25.0%; Pred. No. 2.9e+02;
tive 4; Mismatches 2; Indel8
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Sequence 12, Application US/08191571
Patent No. 5521156
GENERAL INFORMATION:
APPLICANT: Rudlacz, Elizabeth M
APPLICANT: Buck, Stephen H
APPLICANT: Chncincation Merrell Dow Inc.
STREET: P. O. Box 156300 2110 E. Galbraith Rd.
CUNTRY: United States
IP: 45215-6300
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: PRADABLE FORM:
MEDIUM TYPE: PLODS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
OTHER INFORMATION: Core polypeptide US-09-350-641C-1587
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 28, Application US/09620091
Patent No. 6716811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 50.0
Best Local Similarity 25.0
Matches 2; Conservative
                                                                                                                                                                                                   2 GYWLTIWGX 10
                                                                                                                                                                                                                                                            1 GGWASLWNW 9
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2 ESFWVELW 9
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/191,571
FILING DATE: 03-FEB-1994
CLASSIFICATION: 5.4
FILING DATE: 03-FEB-1994
CLASSIFICATION: 5.4
ATTORNEY/AGENT INFORMATION:
NAME: Boudreaux, William R
REGISTRATION NUMBER: 35,796
REFERENCE/DOCKET NUMBER: MO1718
TELEPAX: 213-948-6566
TELEX: 214320
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTER STICS:
LENGTH: 6 amino acids
INFORMATION FOR SEQ ID NO: 12:
CLENGTH: 6 amino acids
TYPE: amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
US-08-191-571-12
Query Match
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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Search completed: January 3, 2005, 17:01:24 Job time : 37 secs

1 YWLR-WG 6

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Sequence 793, App Sequence 837, App Sequence 838, App Sequence 1271, Ap Sequence 154, App

Sequence 69, Appl Sequence 69, Appl Sequence 70, Appl Sequence 70, Appl Sequence 70, Appl Sequence 69, Appl Sequence 69, Appl Sequence 69, Appl Sequence 708, Appl Sequence 181, Appl Sequence 181, Appl Sequence 181, Appl Sequence 187, Appl Sequence 187, Appl Sequence 187, Appl Sequence 187, Appl Sequence 14, Appl Sequence 13, Appl Sequence 523, Appl Sequenc

Sequence:

е 6

Searched:

Database

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Sequence 34, Application US/10046922

Sequence 34, Application US/10046922

Bublication No. US20020164667A1

GENERAL INFORMATION:

APPLICANT: Alitalo, Kari

APPLICANT: Kubo, Hajime

TITLE OF INVENTION: VGGFR-3 INHIBITOR MATERIALS AND METHODS

FILE REFERENCE: 28967/371084A

CURRENT APPLICATION WUMBER: US/10/046,922

CURRENT FILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin version 3.0

LENTH: 10
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5 US-10-182-252A-793

5 US-10-182-252A-833

5 US-10-182-252A-833

7 US-10-182-252A-833

7 US-10-182-252A-833

7 US-08-82-1-39A-92

0 US-08-82-1-39A-92

0 US-08-82-1-39A-92

0 US-08-133-210-70

4 US-10-133-210-70

4 US-10-133-210-70

4 US-10-283-903-69

5 US-10-283-903-69

6 US-10-283-903-69

7 US-10-650-902-181

4 US-10-222-266-708

6 US-10-650-902-181

4 US-10-322-266-34

1 US-10-321-641-1650

4 US-10-31-641-1650

4 US-10-31-641-1650

6 US-10-31-641-1650

7 US-10-31-641-1650

8 US-10-31-641-1650

9 US-09-809-638-440

10 US-09-809-638-440
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100.0%; Pred. No. 0.18;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEX: SITE
LOCATION: (1)..(1)
OTHER INFORMATION: X is any amino acid
NAME/KEX: SITE
LOCATION: (10)..(10)
COCATION: (10)..(10)
COCATION: (10)..(10)
US-10-046-922-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: isolated peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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Sequence 35, Appl
Sequence 1454, Appl
Sequence 1454, Appl
Sequence 8, Appli
Sequence 9, Appli
Sequence 9, Appli
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25.880 Million cell updates/sec
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                             GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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3 US-10-046-922-35
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US-10-133-210-8
4 US-10-371-525-348
4 US-10-371-66-348
4 US-10-371-66-348
4 US-10-371-65-348
5 US-10-182-252A-180
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Maximum Match 100%
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Match Length DB
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Maximum_DB_8eq_length: 10_3
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Publication No. US20030078374A1

GENERAL INFORMATION:
APPLICANT: Proceed Ltd

TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICANTON NUMBER: US/09/572,404B

CURRENT PILING DATE: 2000-05-17

NUMBER OF SEQ ID NOS: 4203

SOFTWARE: ProtPatent version 1.0

SEQ ID NO 1454

LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 10;
                                                                                                                  APPLICANT: KOLVING, BIKKI
APPLICANT: KUDO, Hajime
TITLE OF INVENTION: VGFR-3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 28867/37084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36, Application US/10046922
Publication No. US20020164667A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Kubo, Hajime
TITLE ON INVENTION: VEGER: INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 28967/37084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT PILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PATENTIN version 3.0
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Best Local Similarity 80.0%; Pred. No. 0.18;
Matches 9; Conservative 2; Mismatches
RESULT 2
US-10-046-922-35
Sequence 35, Application US/10046922
Publication No. US20020164667A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: isolated peptide US-10-046-922-35
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Best Local Similarity 50.0
Matches 4; Conservative
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US-10-046-922-36
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US-09-572-404B-1454
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US-10-046-922-36
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LENGTH: 10
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LENGTH: 9
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; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in P2RYS at 139-148 and may interact with Sequence
;) OTHER INFORMATION: in this patent.
US-09-572-404B-1454
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APPLICANT: Berzofsky, Jay
APPLICANT: Berzofsky, Jay
APPLICANT: Gulukota, Kamalakar
APPLICANT: Gulukota, Dennis
APPLICANT: Wang, Zhiping
APPLICANT: Wang, Zhiping
APPLICANT: Anang, Chao
TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
FILER REFRENCE: BU-035AX
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                                                                                                                                                    Length 10;
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APPLICANT: Chestnut, Robert
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Newman, Mark
APPLICANT: Newman, Mark
APPLICANT: Brown, David
ITTLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
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ITTLE OF INVENTION NUMBER: DS/09/894,018
ICURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: DS/06/12-28
PRIOR APPLICATION NUMBER: US 60/173,390
PRIOR APPLICATION NUMBER: US 60/173,390
PRIOR APPLICATION NUMBER: US 60/284,221
PRIOR FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 368
SOFTWARE: FASTERE FASTERE FOR Windows Version 4.0
                                                                                                                                                 57.1%; Score 32; DB 10;
55.6%; Pred. No. 4e+02;
tive 2; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 154, Application US/09894018
Patent No. US20020119127A1
GENERAL INFORMATION:
APPLICANT: EPIMMUNE, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/10133210 Publication No. US20030103964A1
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Best Local Similarity 55.6
Matches 5; Conservative
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US-09-894-018-154
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Length 9;

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Query Match
Best Local Similarity 66.7%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 0.
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US-10-371-069-348
                                 CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/078,904
PRIOR FILING DATE: 1998-05-13
PRIOR PILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 348
CURRENT APPLICATION NUMBER: US/10/371,069
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Publication No. US20030220285A1
GENERAL INFORMATION:
APPLICANT: EPINWUNB Inc.
APPLICANT: Fikes, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Sequence 348, Application US/10371645 , Publication No. US20030216343A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
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APPLICANT: BPINMUNB Inc.
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sette, Alessandro
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Best Local Similarity 66.7°
Matches 4; Conservative
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Publication No. US20030216342A1
GENERAL INFORMATION:
APPLICANT: EPIMMUNE Inc.
APPLICANT: Hermanson, Gary G.
APPLICANT: Hermanson, Gary G.
APPLICANT: Into Sette, Alessandro
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Epimmune Inc.
APP
                                                                                                                                                                     PEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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                                                                                                                                                                                                                                                                                                                                                        Score 30; DB 14; Length 9;
Pred. No. 1.5e+06;
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; OTHER INFORMATION: HIV1 ENV 61 (peptide 25.0032)
US-10-371-525-348
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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; Publication No. US20030203869A1
                                                                                TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
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Best Local Similarity
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4 LTVWGI 9
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4 LTVWGI 9
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GENERAL INFORMATION:
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                                          LENGTH: 9
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66.7%; Pred. No. 1.5e+06;
tive 2; Mismatches 0;
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; OTHER INFORMATION: HIV1 ENV 61 (peptide 25.0032)
US-10-371-645-348
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APPLICANT: BRUNAK, SOREN
APPLICANT: BRUNAK, SOREN
APPLICANT: BRUNAK, SOREN
APPLICANT: BRUNAK, SOREN
APPLICANT: BUUS, SOREN
APPLICANT: BUUS, SOREN
APPLICANT: BUUS, SOREN
APPLICANT: BUUS, SOREN
APPLICANT: LAUEMOLLER, SANNE LISE
APPLICANT: HANSEN, JAN
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
TITLE OF INVENTION NUMBER: US/10/182,252A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: PCT/DK01/0059
PRIOR APPLICATION NUMBER: US 60/179,333
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/179,333
PRIOR APPLICATION NUMBER: US 60/179,333
PRIOR APPLICATION NUMBER: US 60/179,333
PRIOR APPLICATION VUMBER: US 60/179,333
PRIOR APPLICATION UMBER: US 60/179,333
PRIOR PRIOR PRIOR DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1388
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: BRUNAK, SOREN
APPLICANT: BRUNAK, SOREN
APPLICANT: BRUNAK, SOREN
APPLICANT: BUGS, SOREN
APPLICANT: BUGS, SOREN
APPLICANT: BUGS, SOREN
APPLICANT: BUGS, SOREN
APPLICANT: HANSEN, JAN
APPLICANT: BON INVERS: US/10/182,252A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: PCT/DK01/00059
PRIOR APPLICATION NUMBER: US 60/179,333
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1388
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 305
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US-10-182-252A-181
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66.7%; Pred. No. 1.5e+06;
tive 2; Mismatches 0; Indels
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                                                                                                              Sequence 181, Application US/10182252A
Publication No. US20040072162A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 66.7
Matches 4; Conservative
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4 LTVWGI 9
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US-10-182-252A-305
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; Sequence 180, Application US/10182252A
; Publication NO. US20040072162A1
; GENERAL INFORMATION:
    APPLICANT: BRUNK, SOREN
; APPLICANT: BRUNK, SOREN
; APPLICANT: LAUGHOLER, SANNE LISE
; APPLICANT: CORBET, STIVIE
; APPLICANT: LAUGHOLER, SANNE LISE
; APPLICANTON: CONTROL OF HIV INFECTIONS
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS
; CURRENT FILING DATE: 2003-04-10
; PRIOR PELLING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR PILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE PARENT PARENT OF TABLE PARENT NOT 190
; SEG ID NOS: 1388
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                      APPLICANT: Sette, Alessandro

APPLICANT: Sette, Alessandro

APPLICANT: Livingston, Brian

APPLICANT: Livingston, Brian

APPLICANT: Cheanut, Robert W.

APPLICANT: Cheanut, Robert W.

APPLICANT: Epimmune Inc.

TITLE OF INVENTION: Expression Vectors for Stimulating an

TITLE OF INVENTION: Expression Vectors for Guing the Same

FILE REFERENCE: 3996-20022.13

CURRENT APPLICATION NUMBER: US 09/078,904

PRIOR APPLICATION NUMBER: US 09/078,904

PRIOR APPLICATION NUMBER: US 09/078,904

PRIOR FILING DATE: 1998-05-13

PRIOR FILING DATE: 1998-05-15

NUMBER OF SEQ ID NOS: 463

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH.9

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US-10-371-260-348
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ORGANISM: Artificial Sequence
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Hermanson, Gary G.
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Matches 4; Conserv
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4 LTVWGI 9
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Gaps

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Length 9; 0; Indels

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; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide US-10-182-252A-793
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                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1388
SOFWAARE: PatentIn Ver. 2.1
SEQ ID NO 793
LENGTH: 9
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APPLICANT: CORRET, SYLVIE

APPLICANT: LAUGMOLLER, SANNE LISE

APPLICANT: HANSEN, JAN

TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND

TITLE OF INVENTION: CONTROL OF HIV INFECTIONS

CURRENT APPLICATION NUMBER: US/10/182,252A

CURRENT APPLICATION NUMBER: PROMOSO

PRIOR FILING DATE: 2001-01-29

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 1388

SOFTWARE: PARCENT IN OF THE PARCENT OF THE PARCENT
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APPLICANT: FOMSGAARD, ANDERS
APPLICANT: BUNDK, SOREN
APPLICANT: BUNDK, SOREN
APPLICANT: BUNDK, SOREN
APPLICANT: BUNDK, SOREN
APPLICANT: CORBET, STAVIE
APPLICANT: LAUBOLLER, SANNE LISE
APPLICANT: LAUBOLLER, SANNE LISE
APPLICANT: LAUBOLLER, SANNE LISE
APPLICANT: LAUBOLLER, SANNE LISE
APPLICANT: LAUSEN, JAN
TITLE OF INVENTION: HV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
FILE REPERRACE: 0303-04-10
CURRENT APPLICATION NUMBER: US/10/182,252A
CURRENT APPLICATION NUMBER: EP 00610017.6
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-28
PRIOR PILING DATE: 2000-01-28
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US-10-182-252A-792
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                                                                           Query Match 53.6%; Score 30; DB 15; Length 9; Best Local Similarity 66.7%; Pred. No. 1.5e+06; Matches 4; Conservative 2; Mismatches 0; Indels
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; Publication No. US20040072162A1
; GENERAL INFORMATION:
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US-10-182-252A-793
; Sequence 793, Application US/10182252A
; Publication No. US20040072162A1
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ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FOMSGAARD, ANDERS
APPLICANT: BRUNAK, SOREN
APPLICANT: BUUS, SOREN
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Best Local Similarity 66.77
Matches 4; Conservative
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4 LTVWGV 9
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4 LTVWGA 9
US-10-182-252A-305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-182-252A-792
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

January 3, 2005, 16:35:00 ; Search time 38 Seconds (without alignments) 25.320 Million cell updates/sec

US-10-046-922-34 56 1 XGYWLTIWGX 10 Title: Perfect score: Sequence: Scoring table: <arbonius carosum@coring table: dapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

1102 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	escription	glutathione transf	T-cell receptor be	cytochrome-c oxida	gut pentapeptide -		heavy	Ig heavy chain CDR	T-cell receptor be		T-cell receptor be	major fat-globule	>	leucokinin V - Mad	ensin-c	T-cell receptor be	T-cell receptor be	sperm-activating p	hypotrehalosemic h	hypertrehalosemic	hypertrehalosemic	hypertrehalosemic	hypertrehalosemic	hypertrehalosemic	hypertrehalosemic	hypertrehalosemic/	Ig heavy chain DJ	T-cell receptor be	aldehyde ferredoxi	the state of the s
SUMMARIES		8	9	ហ	3	4	6	0	4	7	æ	4	4	D.	0	4	~	7	Ŋ	7	-	80		9	8	1	4	9	e E	4
SU		871868	PT0586	T17075	JH0253	PT0324	PT0289	PT0230	B53284	PT0642	PT0728	B48394	857274	JS0315	A31570	PT0634	PT0562	A60522	B33995	80899	A60421	808998	A26381	JC1416	809138	A31571	PH1344	PH0923	A4075	H37196
	DB	, N	7	~	~	7	~	~	7	~	~	7	7	~	~	~	7	7	~	~	~	~	~	~	~	~	~	~	~	~
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d	Query Match	44.6	41.1	39.3	35.7	35.7	35.7	33.9	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1	32.1
	Score	25	23	22	20	20	20	19	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18
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		nuclease Bh1 (EC 3	T-cell receptor be	T-cell receptor be	locustakinin - mig	T-cell receptor be	T-cell receptor be	glucuronosyltransf	pev-kinin 1 - pena	neuromodulatory pe	neuromodulatory pe	neuromodulatory pe	T-cell receptor be	leucokinin VI - Ma	leucokinin VII - M
F33932	S53789	A59173	PT0629	PT0637	A61068	PT0628	PT0722	PX0008	PD0029	S33244	S33245	S33246	PT0724	JS0316	JS0317
8	~	~	~	~	~	N	~	7	~	~	~	~	~	~	7
10	10	10	ø	9	9	7	7	7	7	7	7	7	ω	œ	80
32.1	32.1	32.1	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4
18	18	18	11	11	17	17	17	11	17	17	17	17	17	17	17
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1 S71868
	glutathione transferase (EC 2.5.1.18) class mu 4 - pig (fragment) N;Alternate names: glutathione S-transferase class mu 4
	C;Species: Sus scrofa domestica (domestic pig)
	C. Accession: 871868
	R;Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J. Riochem . 7 217 879-884 1996
	A,Tille: Characterization of pig liver glutathione S-transferases using HPLC-electrospra
	A;Reference number: S71864; MUID:96332484; PMID:8760377
	A; Molecule type: protein
	A;Residues: 1-10 <rou></rou>
	A, Cross-references: UNIPROT: Q7M3E8
	C; Comment: At least five species-independent classes of cytosolic glutathion transferase
	# MITCOCHONOMIAL FORM ATE KNOWN.
_	C. Compton. C. Studeton.
_	A; Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a
	A, Pathway: detoxification; xenobiotics metabolism
	A, Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism
	es or damage C:Sunerfamily: dlutathione transferase
	C; Keywords: dimer; transferase
	Query Match 44.6%; Score 25; DB 2; Length 10; Beet Local Similarity 75.0%; Pred. No. 4.8e+02;
	Oy 1 XGYW 4
	3 LGYW 6
_	

PRESULT 2
PT0586

PT0586

C; Secies: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: PT0586; PT0592
C; Accession: PT0586; PT0592
B; Peeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A; Reference number: PT0509; MUID:91277601; PMID:1711558
A; Reference number: PT0509
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-7 < PEBS
A; Residues: 1-7 < PEBS
A; Residues: To cell receptor

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A; Reference number: PT0222; MUID:91108337; PMID:1899102
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Best Local Similarity 50.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 XGYWLTIW 8
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4 WISMGGG 10
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Matches 2; Conserv
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3 ITIFGV 8
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                                                   A;Accession: PT0324
A;Molecule type: DNA
A;Residues: 1-9 <YAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: UNIPROT: 079912; EMBL: U82688; NID: 93603112; PID: 93603115; PIDN: AAC622 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 1-5 <UES>
A;Experimental source: gut
C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastr
, and of the circular muscle of the gastro-intestinal junction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PT0324

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JH0253
JH0253
JH0253
gut pentapeptide - Japanese eel
C;Species: Anguilla japonica (Japanese eel)
C;Species: Anguilla japonica (Japanese eel)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
C;Accession: JH0253 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
C;Accession: JH0253 #Ses. Commun. 180, 828-832, 1991
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.
A;Reference number: JH0253; MUID:92062113; PMID:1953755
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     Score 23; DB 2; Length 7;
Pred. No. 2.8e+05;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 66.7%; Pred. No. 2.8e+05; 2; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase
41.1%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 39.3
Best Local Similarity 60.0
Matches 3; Conservative
     Query Match
Best Local Similarity 60.0
Matches 3; Conservative
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SIWGG 7
                                                                                                                                                                                                               6 TIWGX 10
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GFW 3
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Best Local S:
Matches 2
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C.Species: Homo sapiens (man)

C.Species: Jo.Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C.Accession: Pr0289
R.Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
R.Yamada, M.; 395-407, 1991
A.Title: Preferential utilization of specific immunoglobulin heavy chain diversity and jour Reference number: Pr0222; MUID:91108337; PMID:1899102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ig heavy chain CDR3 region (clone 1-118A) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Accession: Pf0230
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and joundation number: Pf0222; MUID:91108337; PMID:1899102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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50.0%; Pred. No. 3.8e+03;
tive 3; Mismatches 0; Indels
                                                                                                   Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain CRD3 region (clone 4-109) - human (fragment)
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                                                                                            Query Match 35.7%; Score 20; DB 2; I Best Local Similarity 37.5%; Pred. No. 2.8e+05; Matches 3; Conservative 2; Mismatches 3;
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A,Residues: 1-10 < YAM>
A,Experimental source: B lymphocyte
C,Keywords: heterotetramer; immunoglobulin
A, Experimental source: B lymphocyte C, Keywords: heterotetramer; immunoglobulin
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A;Residues: 1-10 <YAM>
A;Experimental source: B lymphocyte
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Query Match

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C;Accession: B48394
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
A;Title: Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig II-like sequences.
A;Reference number: A48394; MUID:93250576; PMID:8485470
A;Accession: B48394
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triacylglycerol lipase (EC 3.1.1.3) - Psychrobacter immobilis (fragment)
C;Species: Psychrobacter immobilis
C;Species: Psychrobacter immobilis
C;Species: Psychrobacter immobilis
C;Dacession: S57274
R;Arpigny, U.L.; Feller, G.; Gerday, C.
Biochim. Biophys. Acta 1263, 103, 1995
Biochim. Biophys. Acta 1263, 103, 1995
A;Title: Corrigendum to "Cloning, sequence and structural features of a lipase from the & A;Title: Corrigendum to "Cloning, sequence and structural features of a lipase from the & A;Title: S7274; MUD:95359197; PMID:7632728
A;Accession: S57274
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C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Datesaion: JS0315
R;Hollman, G;M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 27-30, 1987
A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic planatement on JS0315
A;Accession: JS0315
A;Accession: JS0315
A;Accession: JS0315
A;Accession: JS0315
A;Residues: 1-8 <HOL>
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C,Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile acti
C,Keywords: amidated carboxyl end; cephalomyotropic peptide
F;8/Modified site: amidated carboxyl end (Gly) #status experimental
                                                                        C, Species: Cavia porcellus (guinea pig)
C, Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
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                                          major fat-globule membrane protein GP 55 - guinea pig (fragment)
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A;Note: sequence extracted from NCBI backbone (NCBIP:131444)
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Pred. No. 2.8e+05;
1; Mismatches 0
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Best Local Similarity 66.7
Matches 2; Conservative
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                              A;Title: Evolutionarily conserved organization and sequences of germline diversity and A;Reference number: A53284; MUID:91342695; PMID:1678859
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A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
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A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
R;Feeney, A.J.
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0728
R;Peeney, A.J.
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A;Reaidues: 1-4 <HAR>
A;Cross-references: G8:S60737; NID:g233916; PIDN:AAB19518.1; PID:g233918
A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)
C;Keywords: T-cell receptor
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Pred. No. 2.8e+05;
1; Mismatches 0; Indele
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                                                                                                                                                                                                                                                                                                                                                                                                   32.1%; Score 18; DB 2; Length 4; 66.7%; Pred. No. 2.8e+05;
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A;Molecule type: mRNA
A;Residues: 1-7 <FEE.
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor
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A;Molecule type: DNA
A;Residues: 1-7 FFES.
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor
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66.7%;
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Local Similarity 66.7%;
Local Similarity 66.7%;
Immunol. 28, 881-888, 1991
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Matches 2; Conserv
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A; Status: preliminary
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Query Match Best Local 6

Matches

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RESULT 11

GYWLTIWG 9

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T-cell receptor beta chain V-D-J region (121-2CL) - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Accession: PT0634
R.Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A.Riference number: PT0509; MUID:91277601; PMID:1711558
A.Accession: PT0634
A.Accession: PT0634
A.Accession: PT0634
A.Molecule type: mRNA
A.Residues: 1-9 FFEE
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C.Species: Thunnus albacares (yellowfin tuna)
C.Species: Thunnus albacares (yellowfin tuna)
C.Accession: A31570
B.Kohama, Y.; Matsumoto, S.; Oka, H.; Teramoto, T.; Okabe, M.; Mimura, T.
B.Kohama, Y.; Matsumoto, S.; Oka, H.; Teramoto, T.; Okabe, M.; Mimura, T.
B.Kohama, Y.; Matsumoto, S.; Oka, H.; Teramoto, T.; Okabe, M.; Mimura, T.
A.R.Kohama, Y.; Matsumoto, S.; Oka, H.; Teramoto, T.; Okabe, M.; Mimura, T.
A.R.Kohama, Y.; Matsumoto, S.; Owan, H.; Teramoto, T.; Okabe, M.; Mimura, T.
A.R.Kohama, Y.; Matsumoto, S.; Owan, H.; Teramoto, T.; Okabe, M.; Mimura, T.
A.R.Kohama, Y.; Matsumoto, S.; Owan, H.; Teramoto, T.; Okabe, M.; Mimura, T.
A.R.Kohama, Y.; Matsumoto, S.; Owan, H.; Mimura, T.
A.R.Kohama, Y.; Matsumoto, S.; Owan, H.; Mimura, T.
A.R.Kohama, Y.; Matsumoto, S.; Owan, H.; Mimura, T.
A.Kohama, Y.; Matsumoto, S.; Owan, H.; Teramoto, T.; Okabe, M.; Mimura, T.
A.Kohama, Y.; Matsumoto, S.; Owan, H.; Teramoto, T.; Okabe, M.; Mimura, T.
A.Kohama, Y.; Matsumoto, S.; Owan, H.; Teramoto, T.; Okabe, M.; Mimura, T.
A.Kohama, Y.; Matsumoto, M.; Mimura, T.
A.Kohama, M.; Mimura, T.
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A.Kohama, M.; Mimura, T.
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A.Kohama, M.; Mimura, M.; Mimura, M.; Mimura, T.
A.Kohama, M.; Mimura, M.; Mimura, T.
A.Kohama, M.; Mimura, M.; Mimura, M.; Mimura, T.
A.Kohama, M.; Mimura, M
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Job time : 38 secs
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GSGFSSWG 8
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Chloropiast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.
NCBI_TaxID=179915;
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"Characterization of pig liver glutathione S-transferases using HPLC-electrospray-ionization mass spectrometry.";
Biochem. J. 317.099-884(1996).
PIR; S71868; S71868.
GO: GO:0004364; F:glutathione transferase activity; IEA.
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                                                                                                                              "Molecular phylogenetics and mitochondrial genomic evolution in the chamaeleonidae (Reptilia, Squamata)."; Mol. Phylogenet. Evol. 23:22-36(2002).
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-Matchione transferase (EC 2.5.1.18) class mu 4 (Fragment).
Sus scrofa domestica (domestic pig).
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Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
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Pred. No. 1.6e+03;
1; Mismatches 1; Indels
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF44875-3 AAL90547-1; -
GO; GO:0005739; C:mitochondrion; IEA.
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10 AA; 1276 MW; 5E218E2733772727 CRC64;
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                                                                                               MEDLINE=22169767; PubMed=12182400;
Townsend T., Larson A.;
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Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
Phylogeny and evolution of based on three plastid DNA regions.";
Mol. Phylogenet. Evol. 31:277-299 (2004).
EMBL, AM505427.; CAD45547.1;
GO, GO:00003735; F:structural constituent of ribosome; IEA.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
lamiids, Lamiales, Lamiaceae, Nepetoideae, Ocimeae, Fuerstia.
NCBI_TaxID=204226;
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EMBL, AJ505427; CAD45547.1; -. Chloroplast; Ribosomal protein.
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14-MAR-2004 (TrEMBLrel. 27, Created)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                8 AA; 916 MW; DABEAB58637041B5 CRC64;
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                                      SEQUENCE FROM N.A. PubMed=15019625;
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 NCBI_TaxID=204226;
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SEQUENCE FROM N.A.
MEDLINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
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MEDLINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Megaladapidae; Lepilemur.
NCBI_TaxID=78584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Strepsirhini, Megaladapidae, Lepilemur.
NCBI_TaxID=122230;
                                                                                                                                                                                                                                                                                                                                                                                Score 24.5; DB 2; Length 9;
Pred. No. 1.8e+06;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lepilemur edwardsi (Milne-Edwards's sportive lemur).
                                                     Name=COIII;
Lepilemur septentrionalis (northern sportive lemur)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Cytochrome oxidase subunit III (Fragment).
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SEQUENCE 9 AA; 1174 MW; 16C5633636B5045B0 CRC64;
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Last annotation update)
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EMBL; AF224597; AAP33652.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seq
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                                                                                                                                                                                                                                                                                                                                                                               43.8%;
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Best Local Similarity 50.0
Matches 4; Conservative
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Best Local Similarity 50.0
Matches 4; Conservative
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                                                                                 Snyder L.A., Davies J.K., Saunders N.J.;
"Microarray genomocyping of key experimental strains of Neisseria gonorrhoeae reveals gene complement diversity and five new neisserial genes associated with Minimal Mobile Elements.";
BMC Genomics 5:23-23(2004).
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"Miczroarzay genomotyping of key experimental strains of Neisseria
gonorrhoeae reveals gene complement diversity and five new neisserial
genes associated with Minimal Mobile Elements.";
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Neisseriaceae; Neisseria.
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Pred. No. 3.2e+03;
2; Mismatches 1; Indels
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY386266; AAS16521.1; -
                                                                                                                                                                                                                          Saunders N.J.;
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                        BACCBB286379D1A6 CRC64;
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Last annotation update)
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50.0%;
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                                                                                                                                                                                                                                                                                           SEQUENCE 10 AA; 1227 MW;
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MTFWGL 8
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MTFWGL 8
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                                                                   PubMed=15084227;
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 NCBI_TaxID=485;
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SEQUENCE
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AAS16521;
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RESULT 7
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Proc. Natl. Acad. Sci. U.S.A. :
EMBL; AF224636; AAK70595.1; -.
EMBL; AF224637; AAK70599.1; -.
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9 AA; 1160 MW;
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Best Local Similarity
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SEQUENCE
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SEQUENCE
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Pastcrini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;
"Molecular phylogeny of the leamir family cheirogaleidae (primates)
based on mitochondrial DNA sequences.";
Mol. Phylogenet. Evol. 19:45-56(2001).
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=21184272; PubMed=11286490;

MEDLINE=21184272; PubMed=11286490;

Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;

"Molecular phylogeny of the lemur family cheirogaleidae (primates)
based on mitochondrial DNA sequences.";

Mol. Phylogenet. Evol. 19:45-56(2001).
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SEQUENCE FROM N.A.
MEDLINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=22631563; PubMed=12719521;
Pastocrini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A.
MEDLINE=22281620; PubMed=12393004;
MEDLINE=22281620; Porstner M.R., Martin R.D.;
Pastorini J., Forstner M.R., Martin R.D.;
"Phylogenetic relationships among Lemuridae (Primates): evidence from "Phylogenetic relationships"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                           Mitochondrion.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Strepsirhini, Daubentoniidae,
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Mammalia, Eutheria, Primates, Strepsirhini, Cheirogaleidae,
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Cytochrome oxidase subunit III (Fragment). Name=COIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER 1 1
SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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BMB1; AF224641; AAK70615.1; -
EMB1, F224642; AAK70619.1; -
GO, GO:0005739; C:mitochondrion; IEA.
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                                                                                                  Daubentonia madagascariensis (Aye-aye)
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SEQUENCE FROM N.A.
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Pastcrini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;
"Molecular phylogeny of the lemur family cheirogaleidae (primates)
based on mitochondrial DNA sequences ";
Mol. Phylogenet. Evol. 19:45-56(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
                                                                                                                                                                                                                                                                                                                                         Gaps
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mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;
Microcebus.
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Pred. No. 1.8e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                               Length 9;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit III (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                        9 AA; 1160 MW; D5C563636B5045A2 CRC64;
Acad. Sci. U.S.A. 100:5879-5884 (2003)
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Pred. No. 1.8e+06;
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                                                                           EMBL, AF224638; AAK70603.1; -.
EMBL, AF224639; AAK70607.1; -.
GO, GO:0005739; C:mitochondrion; IEA.
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EMBL; AF224631; AAK70575.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
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YWLTIWGX 10
                           5 YW---WGS 9
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                                                                                                           MEDLINE=21184272; PubMed=11286490;
Pastcrini J., Martin R.D., Ehreemann P., Zimmermann E., Forstner M.R.;
"Molecular phylogeny of the lemur family cheirogaleidae (primates)
based on mitochondrial DNA sequences.";
Mol. Phylogenet. Evol. 19:45-56 (2001).
                                                                                                                                                                                               MEDLINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21396409; PubMed=11504862;
Shao R., Campbell N.J., Schmidt E.R., Barker S.C.;
"Increased rate of gene rearrangement in the mitochondrial genomes of
three orders of hemipteroid insects.";
Mol. Biol. Evol. 18:1828-132(2001).
EMBL; AF335990; AAK55283.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                  Bukaryota; Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;
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Neoptera; Paraneoptera; Hemiptera; Buhemiptera; Heteroptera;
Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;
                                                                                                                                                                                                                                                                                                                                                                                                    Length 9;
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Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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SEQUENCE 9 AA; 1206 MW; A2C563636B5041A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UDN-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome c oxidase subunit III (Fragment).
                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884 (2003).
EMBL; AF224624; AAK70547.1; -...
EMBL; AF224625; AAK70551.1; -...
EMBL; AF224627; AAK7055.1; -...
EMBL; AF224627; AAK70559.1; -...
EMBL; AF224628; AAK70559.1; -...
EMBL; AF224628; AAK70567.1; -...
GO, GO. 0005739; C.mitochondrion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                  43.8%; Score 24.5; DB 2; 50.0%; Pred. No. 1.8e+06; ative 1; Mismatches 0;
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           Microcebus murinus (Lesser mouse lemur)
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Matches 4; Conservative
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                                                                     NCBI_TaxID=30608;
                        Mitochondrion.
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                                                            Microcebus.
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Gaps
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Townsend T., Larson A.;
"Molecular phylogenetics and mitochondrial genomic evolution in the chamaeleonidae (Reptilia, Squamata).";
Mol. Phylogenet. Evol. 23:22-36(2002).
                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae;
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Pred. No. 4.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Townsend T.M., Larson A.L.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF448730; AALS9472.1; -
GO; GO:0005739; C:mitochondrion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 10
10 AA; 1327 MW; 5E2180C7336415B7 CRC64;
                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                    Bradypodion tavetanum (Dwarf Fischer's chameleon)
10 AA
                                                                                                                Cytochrome c oxidase subunit I (Fragment).
Name=COI;
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PRT;
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PRELIMINARY;
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

December 30, 2004, 12:55:07 ; Search time 69.6226 Seconds (without alignments) 51.525 Million cell updates/sec Run on:

US-10-046-922-35 72 1 CGYWLTIWGC 10 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2002273 seqs, 358729299 residues Searched:

Total number of hits satisfying chosen parameters:

2002273

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A Geneseq 23Sep04:* 1: geneseqp1980s.* geneseqp1980s:* geneseqp1990s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp20048:*

## SUMMARIES

Dearrintion		٠	Abp53931 VEGFR-3 b	Abp53968 VEGFR-3 b	Adc87481 Human GPC	Adc99638 Cancer-re	Aao26074 Fc region	Adj50741 Human ser	5	Aau90545 Insulin/i	Aay59880 Human nor	Abu49938 Protein e	Abb04861 LDL recep	Adp29850 Human sec	Aae31487 Human but	Aau91293 Human NOV	Aao26093 Fc region	_	Abp73979 Candida a	Abu30004 Protein e	Adc97318 E. faeciu	Adl81869 P. aerugi	Aay94989 Human sec	Abb90081 Human pol	Aao17173 Human sec	Abg64784 Human alb
		ABP53932	ABP53931	ABP53968	ADC87481	ADC99638	AA026074	ADJ50741	ADM87650	AAU90545	AAY59880	ABU49938	ABB04861	ADP29850	AAE31487	AAU91293	AA026093	ADJ50760	ABP73979	ABU30004	ADC97318	ADL81869	AAY94989	ABB90081	AA017173	ABG64784
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Query	1000	100.0	75.0	69.4	0.99	65.3	63.9	63.8	63.9	62.5	62.5	62.5	61.8	61.1	61.1	61.1	59.7	59.7	59.7		59.7	59.7	59.0	59.0	59.0	59.0
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ADL78051 AAR66278 AAB12156	AAM78581 AAB73100 AAB7198 ABG64785 ABG647805	ADNO5188 AAM25822 ABB12006 AAM79565	ABO07116 ABB04863 AAY16572 AAY41668	AAY06596 AAB20122 AAB20123 ADD32192
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## ALIGNMENTS

Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; anglogenesis; lymphangiogenesis; vascular endothelial growth factor; cytoëtatic; hepatotropic; antiinflammatory; hypotensive; antiidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypetrension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor. VEGFR-3 binding peptide SEQ ID NO:35. Ŕ ABP53932 standard; peptide; 10 16-JAN-2002; 2002WO-IB000099. 17-JAN-2001; 2001US-0262476P. (first entry) WO200257299-A2. Homo sapiens. 09-JAN-2003 25-JUL-2002. Synthetic. ABP53932; RESULT 1 ABP53932 

(LUDW-) LUDWIG INST CANCER RES. (LICN ) LICENTIA LTD.

Alitalo K, Koivunen E, Kubo H;

WPI; 2002-691521/74.

New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.

Claim 13; Page 80; 149pp; English.

The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

spleen, kidney, lymph node, small intestine, blood cells

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antiidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
                                    ovary,
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                        pancreas, colon, stonach, breast, endometrium, prostate, testicle, ovary skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
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spleen, kidney, lymph node, small intestine, blood cells,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEGFR-3 binding peptide SEQ ID NO:34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP53931 standard; peptide; 10 AA
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                                                                                                                                                                                                                                                                                                                                                     10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              1 CGYWLTIWGC
                                                                                                                                                                                                                                                                                                                                                                                                                                               CGYWLTIWGC
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                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                  present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                     Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200257299-A2
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                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FICN )
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                                                                                                                                                                                                                                                                                                                                                     Matches
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ABP 3931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotenaive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the present invention
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                       ;
                                                                                                                                                                      Length 10;
                                                                                                                                                                                                       0; Indels
                                                                                                                                                                    DB 5;
0.67;
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                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                    75.0%; Score 54; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEGFR-3 binding peptide SEQ ID NO:73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 147; 149pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    ABP53968 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JAN-2002; 2002WO-IB000099.
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                                                                                                                                                                                                       8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LUDW-) LUDWIG INST (LICN) LICENTIA LTD.
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                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                            2 GYWLTIWG
                                                                                                                                                                                                                                                                           GYWLTIWG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                    Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                       ABP53968;
                                                                                                                                                                       Query Match
                                                                                                                                                                                          Best Loc
Matches
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Cancer-related Tie-1-binder peptide - SEQ ID 476.

(first entry)

01-JAN-2004

ADC99638;

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ADC99638 standard; peptide; 25

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RESULT 5
ADC99638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The protein sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
         pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a VEGFR-3 binding peptide, which is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
                                                                                                                                                                                                                                                                                                                          GPCR; guanosine triphosphate-binding protein coupled receptor;
                                                                                                                                   Gaps
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small intestine, blood cells,
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                                                                                                           Score 50; DB 5; Length 10; Pred. No. 2.3;
                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCI & TECHNOLOGY
                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aburatani H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; SEQ ID NO 1934; 28pp; English.
spleen, kidney, lymph node,
                                                                                                                                                                                                                                   ADC87481 standard; protein; 304 AA
                                                                                                                                                                                                                                                                                                    Human GPCR protein SEQ ID NO:1934.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NAAD-) NAT INST ADVANCED IND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Asai K, Akiyama Y,
                                                                                                          69.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUN-2002; 2002EP-00013517
                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUN-2001; 2001JP-00246789
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                                                                                                                                                                                                                                                                              (first entry)
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Best Local Similarity 60.0
Lange 6; Conservative
                                                                                                                                 6; Conservative
                                                                                                                                                        1 CGYWLTIWGC 10
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                                                                                                                                                                           1 CGYWXXXWXC
                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 304 AA;
                                                                                     Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                               EP1270724-A2
                                                                                                                                                                                                                                                                                                                                       gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ADSC-)
                                                                                                                                                                                                                                                                                                                          human;
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ID ADC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Selecting target and target binder pairs for preparing a composition for treating cancer by mixing in a reaction vessel phage expressing biological targets and phage expressing target binders.
cytostatic; cancer; gene therapy; DGI-2; DGI-5; DGI-7; DGI-9; Hras; leptin; VEGF; vascular endothelial growth factor receptor; VEGF-R1; VEGF-R2; VEGF-R3; FLT1; PMS-related tyrosine kinase 1; FLK1; KDR; KLIASE insert domain protein receptor; EGFR; epidermal growth factor; RGFR1; fibroblast growth factor; Tie-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 13;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 26; SEQ ID NO 476; 172pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spruyt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAO26074 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DGIB-) DGI BIOTECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                       24-OCT-2001; 2001US-0345471P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.3%;
                                                                                                                                                                                                                                                                                                                                               24-OCT-2002; 2002WO-US034021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goldstein N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-APR-2003 (first entry)
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                                                                                                                                                                                                                               WO2003035839-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pillutla RC, B:
Prendergast J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25 AA;
                                                                                                                                                                          Unidentified.
                                                                                                                                                                                                                                                                                       01-MAY-2003
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WPI; 2004-082161/08
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or
                                                                                                                                                                                                                              The invention relates to novel isolated polypeptides comprising a sequence that binds an immunoglobulin Fc region. The polypeptides are useful as binding molecules for detecting, isolating or purifying immunoglobulin Fc-region polypeptides present in a solution, e.g. whole blood, plasma or transgenic milk. The Fc-region binding polypeptides are also useful for regulating or preventing an antibody response, or for increasing the half-life and over all stability of a therapeutic or diagnostic compound that is administered to or enters the circulatory system of an individual. This sequence represents an Fc region binding
Immunoglobulin Fc region; binding; whole blood; plasma; transgenic milk;
antibody response; half-life; stability; circulatory system.
                                                                                                                                                                           isolating
solution,
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                        Potter MD;
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                                                                                                                                                                         polypeptides, useful as binding molecules for detecting, ifying immunoglobulin Fc-region polypeptides present in a regulating or preventing an antibody response.
                                                                                                                                                                                                                                                                                                                                                      63.9%; Score 46; DB 6; Length 17; 66.7%; Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human serum albumin; HSA; serum; blood; tumour; human.
                                                                                                                                       Ransohoff TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human serum albumin binding peptide, Seq ID No 278.
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                        Stochl M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADJ50741 standard; peptide; 17 AA
                                                                                                                                                                                                               Claim 3; Page 76; 152pp; English
                                                                                  18-APR-2002; 2002WO-US012492.
                                                                                                    18-APR-2001; 2001US-0284534P.
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                                                                                                                                        Ley AC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                        Conservative
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CGFWPRIWG 12
                                                                                                                                                                                                                                                                                                                                                                                         1 CGYWLTIWG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sato AK, Dawson BM;
                                                                                                                                                         WPI; 2003-201220/19
                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORP
                                                                                                                     (DYAX-) DYAX CORP
                                                                                                                                        Rondon IJ, Wu Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003106493-A1
                                                                                                                                                                                                                                                                                                                                     Sequence 17 AA;
                                             WO200286070-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DYAX-) DYAX
                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-DEC-2003.
                                                               31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADJ50741;
                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                          The invention relates to a method of evaluating sample by providing a soluble serum protein (I), one or more compounds physically associated with (I), and a (II-binding agent that comprises a peptide that specifically binds to (I) allowing the (I)-binding agent to bind to to form a complex including one or more compounds physically associated sample, and evaluating one or more of the physically associated compounds. The sample complex from one or more components of the sample comprises blood or serum, or is obtained from a biopsy. The sample may also be obtained from a tumour or a region within modulate interaction of serum protein-binding compound and serum protein and for identifying binding ligands for serum protein. The present sequence represents a serum albumin-binding peptide identified using the
Evaluating sample comprising soluble serum protein by forming complex comprising serum protein and physically associated compounds using peptide ligand that specifically binds with proteins, which is separated and evaluated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       respiratory; cytostatic; antiarthritic; antiinflammatory; gastrointestinal; antibacterial; immunosuppressive; antidiabetic; antirheumatic; gene therapy; molecular weight marker; chromosome marker; chromosome tag; genetic fingerprinting; nutritional supplement; cancer; inflammatory condition; arthritis; inflammatory bowel disease; crohn's disease; sepsis; rheumatord atthritis; diabetes mellitus type 1; graft versus host disease; human; expressed sequence tag; EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotides and polypeptides, useful for treating, e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human EST derived amino acid sequence SEQ ID NO:743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang J, Ren F, Xue
D, Zhao QA, Wang Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                              Disclosure; SEQ ID NO 278; 191pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADM87650 standard; protein; 136 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-2002; 2002WO-US022858.
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28-MAR-2002; 2002US-00112944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.9%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yang Y, Weng G,
Ghosh MJ, Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         method of the invention.
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CGFWPRIWG 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CGYWLTIWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADM87432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004009834-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADM87650;
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WO200172771-A2

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comprising a nuclectioe sequence selected from SEQ ID NO:1-244, or (b) comprising a nuclectide sequence selected from SEQ ID NO:1-244, or (b) comprising a nuclectide sequence selected from SEQ ID NO:1-244, or (b) comprising a nuclectide sequence selected from SEQ ID NO:1-244, or high encodes a polypeptide with biological activity, where the polynuclectide hybridiaes to (I) under stringent hybridiaeticor.

CC or has greater than 99% sequence identity with (I). (I) has respiratory, antibacterial, immunosuppressive, antidiabetic and antirheumatic cryostatics, and can be used in gene therapy. (I) can be used for generating polynucleotides encoding chieric or fusion proteins and heterologous protein sequences. The polynucleotides can be used for carporating polynucleotides encoding chieric or sexpess recombinant protein for analysis, characterisation or therapeutic use; as markers for tagsues in which the corresponding protein is protein or sexpess recombinant protein for analysis, characterisation or therapeutic use; as markers for tagsues in which the corresponding protein is checked by sequences; as molecular weight markers on gene; as markers for genetic disorders; as source of information to derive PCR configurations, to compare with endogenous DNA sequences in the process of identify protein or expression patterns; to raise antiport including for examination of expression patterns; to raise antiport including for examination of expression patterns; and as antigen protein antibodies using DNA immunisation techniques; and as an antigen protein antibodies or elicit another immune response. The polynucleotides and polypeptides can also be used as nutritional sources or supplements, e.g. as a protein or animo acid supplement, as a currer of supplements, e.g. as a protein or endogeneration of treater closure of non-healing wounds, for the generation and treatment of lung or liver fibrossis, compositions are useful for promotices can also be used to treat cronditions real nutries and polypeptides can also be used as 
cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease, Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
                                                                                                                                                            present invention describes an isolated polynucleotide (I): (a)
                                                                                                     Example 2; SEQ ID NO 743; 591pp; English.
                                                         versus host disease.
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AAY59880;
                                                                    RESULT 10
                                                                                           AAY59880
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                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; antidiabetic; neuroprotective; cerebroprotective; ophthalmological; insulin; receptor; gene therapy; diabetes; insulin-like growth factor-l; IGF-l; tumour; prostere; breast; diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.
                                                                    Gapa
                                                                                                                                                                                                                                                                                                                                                                                          Insulin/insulin-like growth factor receptor-binding peptide #2501
                                                                    ö
                      Score 46; DB 8; Length 136;
Pred. No. 73;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                             AAU90545 standard; peptide; 20 AA.
                        63.9%;
60.0%;
                                                                                                                                                                                                                                                                                                                                               (first entry)
Query Match
Best Local Similarity 60...
6; Conservative
                                                                                                                                                     93 CGRWDWLWGC 102
                                                                                                            1 CGYWLTIWGC 10
                                                                                                                                                                                                                                                                                                                                                  18-JUN-2002
                                                                                                                                                                                                                                                                                                     AAU90545;
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RESULT 9

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Sequence 136 AA;

(META-) METAGEN GES GENOMFORSCHUNG MBH.

Synthetic

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The invention relates to a method of modulating insulin activity in mammalian cells by administering a peptide that binds the insulin receptor (IR). A composition containing a peptide, optionally expressed from gene therapy vectors, that binds to Site I of IR and an insulin agonist are useful for treating diabetes. Also, peptides that are antagonists of the insulin-like growth factor-I (IGF-1) receptor are useful for treating insulin-like growth factor (IGF-1) receptor are useful for treating insulin-like growth factor (IGF-) sensitive tumours (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1 receptor agonists are useful for treating neurological diseases, including stroke and diabetic neuropathy. The peptides are also useful in exceptor agonists and research reagents. Adusso34-Adus09557 represent IR and/or IGF-1 receptor-binding peptides and related amino acid sequences of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer; treatment; anticancer; cytostatic; gene therapy; sequence tag.
                                                                                                                                                                                                                                                           Modulating insulin activity in mammalian cells, for treating e.g. diabetes and tumors, comprises using peptides that bind to insulin or insulin-like growth factor receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                     Brandt J;
, Mandecki WS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Length 20;
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                                                                                                                                                                   Pillutla R, B
Ostergaard S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human normal uterus tissue derived protein 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB 5
Pred. No. 20;
0; Mismatches
                                                                                                                                                                     Schaeffer L,
J, Cheng W,
                                                                                                                                                                                                                                                                                                                         Disclosure, Fig 8-3; 390pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY59880 standard; protein; 129 AA.
                                                                                                                    (DGIB-) DGI BIOTECHNOLOGIES LLC (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                 Beasley J, Blume AJ, Schaeffe.
Brissette R, Spetzler J, Chen;
Hansen PH, Ravera M, Hsiao K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.5%;
60.0%;
                                                           29-MAR-2000; 2000WO-US008528
                                                                                    29-MAR-2000; 2000WO-US008528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CGYWLTIWGC 10
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 AA;
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EST; expressed
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                            04-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
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This invention describes novel CDNA sequences (A) highly expressed in normal uterine tissue which can have anticancer and cytostatic activity and can be used for gene therapy. (A) are used (1) for recombinant expression of polyapptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of uterine cancer; (ii) directly for treating this form of cancer including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling ESTB (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTB from different libraries may represent different parts of the same cunknown gene, discorting the estimated frequency of cocurrence in a particular tissue. ANYS9838-YS9832 represent protein fragments encoded by the human uterine tissue derived CDNA fragments represented in AAZ41325-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                          New nucleic acid sequences expressed in normal uterine tissues, and derived polypeptides, for treatment of uterine cancer and identification of therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense; prokaryotic essential gene; cell proliferation; drug design.
             Dahl E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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           Schmitt A, Pilarsky C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.5%; Score 45; DB 2; Length 129; 62.5%; Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by Prokaryotic essential gene #35465.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
             Hinzmann B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU49938 standard; protein; 828 AA.
                                                                                                                                                         Claim 23; Page 138; 154pp; German.
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342921P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 62.5
             Specht T,
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Trawick JD,
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CSHWLTVW 39
                                            WPI; 1999-591956/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CGYWLTIW 8
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N-PSDB; ACA53808.
                                                             N-PSDB; AAZ41339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yersinia pestis.
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           Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU49938
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Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
ABU49938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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c. The invention relates to an isolated nucleic acid compitibing any one of the 6213 antisense sequences given in the specification where expression to the 6213 antisense sequences given in the specification where expression to the nucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated to polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibited by the attisted polypeptide or the activity of a gene in an operon required for proliferation or that activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation or that the hast callular proliferation of the gene product or that the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibicing collectation of an organism acts; (9) manufacturing an antibicing or the biological compound's activity; (11) a culture comprising strains in which each of the strains is present in a culture or collection of product is overexpressed, or underexpressed; (10) profiling a compound that inhibits the compound that inhibits the compound activity; (11) a culture comprising strains in which each of the strains is present in a culture or collection of confidentifying the target of a compound that inhibits the confidentifying proteins or screening for homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, cell antifying prokaryotic essential genes. Note: The sequence is encoded by one of the target promit discovery programming general sequence is encoded by one of the target promit discovery programming general sequence is encoded to the target promit discovery programming and pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
                   New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Low density lipoprotein receptor binding protein; signal transduction;
LDL receptor binding protein; LDL receptor signalling pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                              invention relates to an isolated nucleic acid comprising any
                                                                 isolate candidate molecules for rational drug discovery programs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.5%; Score 45; DB 6; Length 828
58.3%; Pred. No. 4.6e+02;
ive 1; Mismatches 2; Indels
                                                                                                                SEQ ID NO 77862; 1766pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity be...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372 CGLWLELLSWGC 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CGYWLTI -- WGC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 828 AA;
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                                                                                                                  Claim 25;
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17-SEP-2002;
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17-SEP-2002;
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17-SEP-2002;
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02-MAY-2003;
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                                                                                                                                                         17-SEP-2002;
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  The present invention describes a method for detecting a stress that alters a functional interaction of a low density lipoprotein (LDL) receptor binding protein (1) with an LDL receptor interaction domain (II). The method involves introducing a predetermined stress into a system which provides a stress-biased physical interaction of (I) with contact of the stress, the system provides an unbiased interaction of (I) and (II), and detecting the stress-biased interaction of (I) and (II), where in the absence of the stress, the system provides an unbiased interaction of (I) and (II), where a difference between BI and UI indicates that the stress alters the interaction of (I) and (II). (I) is selected from of (I) and (II), where a difference between BI and UI indicates that the stress alters the interaction of (I) and (II). (I) is selected from the stress that alters functional interaction of LDL receptor binding polypeptide with LDL receptor interaction domain. The method is useful for detecting and modulating signal transduction through LDL receptors. ABBO4778 to ABBO4909 represent LDL receptor binding proteins which are used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
                                                                    Detecting stress that alters interaction of LDL receptor binding polypeptide with LDL receptor interaction domain, comprises detecting difference in stress-biased and unbiased interaction of peptide and domain in a system.
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                   61.8%; Score 44.5; DB 5; Length 1024; 54.5%; Pred. No. 6.5e+02; ive 3; Mismatches 1; Indels 1
                                                                                                                                Disclosure; Page 148-150; 200pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein SEQ ID #617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP29850 standard; protein; 149 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-AUG-2002; 2002US-0406576P.
29-AUG-2002; 2002US-04065879P.
29-AUG-2002; 2002US-0406588P.
29-AUG-2002; 2002US-0406688P.
29-AUG-2002; 2002US-0406611P.
29-AUG-2002; 2002US-0406611P.
29-AUG-2002; 2002US-0406611P.
29-AUG-2002; 2002US-0406616P.
29-AUG-2002; 2002US-0406640P.
29-AUG-2002; 2002US-0406640P.
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(TEXA ) UNIV TEXAS SYSTEM
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Best Local Similarity 54.5-
Best Gonservative
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892 CGHWIETMWDC 902
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                        Gotthardt M;
                                               WPI; 2002-082855/11.
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                        Herz J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
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New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 2002US-04110B2P
2002US-0411101P
2003US-0463101P
2003US-0463700P
2003US-046370BP
2003US-0463716P
2003US-0463712P
2002US-0410947P.
2002US-0410948P.
2002US-0410949P.
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2003US-0467203P
2003US-047130EP
2003US-047130EP
2003US-0471336P
2003US-0472420P
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2002US-0410957P.
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2002US-0411055P.
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17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
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17-SEP-2002;
17-SEP-2002;
18-APR-2003;
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17-SEP-2002;
17-SEP-2002;
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18-APR-2003;
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22-MAY-2003;
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17-SEP-2002;
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02-MAY-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to B7-H1.2 or Butryophilin 2/3 polypeptides of human B7 polypeptide family and polynucleotides encoding such proteins. Sequences of the invention are useful for treating an immunological conditions (e.g., transplant rejection, graft-versus-host disease, allergy, asthma, inflammatory bowel disease, sepsis), diseases that are caused or exacerbated by T-cell mediated inflammation (e.g., Alzheimer's disease or atherosclerosis), autoimmune diseases (e.g., systemic lupus erythematosus, autoimmune dabetes, diabetic neuropathy, theumatoid authities sclerosis, autoimmune diabetes, diabetic neuropathy, theumatoid arthritis), bacterial or viral infections ench as human immunodeficiency virus (HIV) infection, delayed reconstitution of T-cells, defects in T-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New B7-H1.2 or Butryophilin 2/3 polypeptide of the human B7 polypeptide family, useful for treating an immunological condition e.g. transplant
encoding a polypeptide which is believed to be cytostatic, antifalmatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present svailable on WIPOWEB and is not in the specification.
                                                                                                                                                               Gaps
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                                                                                                                                   Length 149;
                                                                                                                                                            1; Indels
                                                                                                                                   61.1%; Score 44; DB 8; I
62.5%; Pred. No. 1.5e+02;
ive 2; Mismatches 1;
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                                                                                                                                                                                                                                                                                     AAE31487 standard; protein; 166 AA.
                                                                                                                                                                                                                                                                                                                                                                   Human butryophilin 2/3 protein.
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19-JAN-2001; 2001US-0262737P.
07-JAN-2002; 2002US-00260617.
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                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                Local Similarity 62.5
hes 5; Conservative
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CHFWLTVW 102
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                                                                                                           Sequence 149 AA;
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cell or accessory cell function or congenital immunodeficiencies. They are also used in gene therapy. The present sequence is human butryophilin
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Patturajan M;
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                                                                                                                                           Length 166;
                                                                                                                                         Score 44; DB 6; Length 166
Pred. No. 1.6e+02;
1; Mismatches 2; Indels
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Rastelli L, Verney CAM,
Taupier RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                 AAU91293 standard; protein; 415 AA.
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2000US-0228324P.
2000US-0228997P.
2000US-0229185P.
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2000US-0229848P.
2000US-0229850P.
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31-JAN-2001; 2001US-026551BP.
15-MAR-2001; 2001US-0276451P.
27-MAR-2001; 2001US-0279196P.
                                                                                                                                              61.1%;
62.5%;
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Zerhusen BD, Ra
, Padigaru M, 1
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                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                         127 YWEVVWGC 134
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                                                                                                                                                                    Best Local Similarity
Matches 5, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human NOV8 protein
                                                                                                                                                                                                                                            3 YWLTIWGC
                                                 consensus protein
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                                                                                                   Sequence 166 AA;
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01-SEP-2000;
01-SEP-2000;
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25-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spytek KA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU91293;
                                                                                                                                                Query Match
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the invention relates to an isolated of your and to be controlled are a controlled to a secreted polypeptide, of the mature form of NOVI, 2a, 2b, 3b, 3b, 5c, 5d, 5d, 5f, 5g, 5h, 5i, 6, 7 and 8), a variant of NOVX, a controlled are a coll comprising the vector. an anti-NOVX anticlody, determining the presence of NOVX in a sample using the anticlody, determining the presence of NOVX oblymuclecide in a sample using a probe which binds to NOVX polymuclecide. In a sample using a probe which binds to NOVX polymuclecide, identifying a an agent which binds to C determining the presence of NOVX bolymuclecide in a sample using a probe which binds to NOVX bolymuclecide. In a sample using a probe which binds to NOVX polymuclecide, identifying a an agent which binds to NOVX including modulators of NOVX. NOVX, the polymuclecide and the cardiomyopathy, atherosclerosis, associated disorder selected from cardiomyopathy, atherosclerosis, casecolated associated associated associated selected from cardiomyopathy, atherosclerosis, casecolated associated and neuropsychiatric disorders, hypertension, wound craning associated and the antibody are useful in screening assays, detection assays (e.g., chromosomal mapping, issue typing, forensic bology), coperated pharmacogenomic), and in methods of treatment (e.g., therapeutic and prophylactic). NOVX is useful as treatment (e.g., chromosomal mapping, tasue typing, forensic bology), copredictive medicine (e.g., diagnostic assays, prognostic assays, prognostic assays, continuing and pharmacogenomic), and in methods of treatment (e.g., therapeutic and prophylactic). NOVX as vaccines to recent for potential agonist and antagonist compounds, and as batt of the acting non-human t The invention relates to an isolated cytoplasmic, nuclear, membrane bound 

Sequence 415 AA;

0; Gaps 61.1%; Score 44; DB 5; Length 415; 62.5%; Pred. No. 3.5e+02; ive 2; Mismatches 1; Indels Query Match
Best Local Similarity 62.5
Matches 5; Conservative

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| :|||:| 95 CHFWLTVW 102 1 CGYWLTIW 8

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Search completed: December 30, 2004, 13:07:53 Job time : 72.6226 secs

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us-10-046-922-35.rai

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LENGTH: 1024
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Sequence 46926, A
Sequence 9, Appli
Sequence 3, Appli
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                                                                                                      December 30, 2004, 12:59:07; Search time 23.0189 Seconds (without alignments) 28.810 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 367,
Sequence 3, Ap
Sequence 3, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10,
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
               GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-425-043-3
US-08-836-325-10
                                                                                                                                                                                                                                                                                         478139 segs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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No.
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Sequence 6945, Application US/09107532A
; Sequence 6945, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ï
                                                      12, Appl
11, Appl
12, Appl
7, Appli
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19350, A
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                                                                     Sequence 11,
Sequence 12,
Sequence 7,
                                                         Sequence 12,
                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Sequence Synthetic US-09-562-737-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                              Sequence 84, Application US/09562737
Sequence 84, Application US/09562737
GENERAL INFORMATION: CAPPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE ROF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT PILIOR DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7110
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
US-09-457-571-10
US-09-028-4
US-09-028-4
US-09-02-02-4
US-08-816-325-11
US-08-816-325-12
US-09-457-571-11
US-09-457-571-12
US-09-457-571-7
US-09-457-571-7
US-09-634-907A-2
US-09-816-994-2
US-09-816-994-2
US-09-816-994-2
US-09-816-994-2
US-09-816-994-2
US-09-816-994-2
US-09-816-994-2
US-09-816-996-4
US-09-816-996-4
US-09-818-996-4541
US-09-443-041A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44.5; DB 4;
Pred. No. 1.6e+02;
3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.8%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 61.8
Best Local Similarity 54.5
Matches 6; Conservative
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 RESULT 2
US-09-107-532A-6945
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Sequence 3, Application US/09354147C

Sequence 3, Application US/09354147C

Patent No. 6573067

GENERAL INFORMATION:

APPLICANT: Dib-Haj; Sulayman

APPLICANT: Waxman, Stephen G.

TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia

FILE REFERENCE: 44574-5004-01-US

CURRENT FILING DATE: 1999-07-16

PRIOR PLING DATE: 1998-01-29

PRIOR FILING DATE: 1998-01-29

PRIOR FILING DATE: 1998-01-29

PRIOR FILING DATE: 1998-01-29

PRIOR FILING DATE: 1998-01-29

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3

LENGTH: 1765
                                                                             APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Maxman, Stephen G.
TITLE OF INVENTION: Modilation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-05
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1999-07-16
PRIOR PPLICATION NUMBER: US 60/072,990
PRIOR PILING DATE: 1998-01-29
PRIOR PILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR PILING DATE: 1998-11-20
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 2
LENGTH: 1765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (652)..(1334)
OTHER INFORMATION: Xaa at position 652 is Leu; Xaa at position 1334 is Asn
OTHER INFORMATION: or Lys. Xaa's result from n's in SEQ ID NO: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 59.0%; Score 42.5; DB 4; Length 1765; Best Local Similarity 54.5%; Pred. No. 5.1e+02; Matches 6; Conservative 2; Mismatches 1; Indels 1
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         Sequence 2, Application US/09354147C Patent No. 6573067 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Rattus norvegicus
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ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: UNSURE
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Best Local Similarity 54.5
Matches 6; Conservative
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754 CGEWIENMWGC 764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.7%; Score 43; DB 4; Length 492; 85.7%; Pred. No. 1.3e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 86, Application US/09562737;
Patent No. 6428967;
GENERAL INPORMATION:
APPLICANT: Herz, Joachim;
APPLICANT: Gotthardt, Michael;
TITLE OF INVENTION: LDL Receptor Signaling Pathways;
FILE REFERENCE: UTSW0708
CURRENT FILING DATE: 2000-05-01;
NUMBER OF SEQ ID NOS: 132;
SOFWWARE: Patentin Ver. 2.1
SEQ ID NO 86
              SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                              ATORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 47C-012
TELEPRONEY (781)893-507
TELEPRONEY (781)893-507
TELEPRONEY (781)893-507
TELEPRONEY (781)893-627
INFORMATION FOR SEQ ID NO: 6945:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: AUDICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...492
SEQUENCE DESCRIPTION: SEQ ID NO: 6945:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecium
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.0%;
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Best Local Similarity 63.6.
The Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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Sequence 3, Application US/09792616

Sequence 3, Application US/09792616

Sequence 3, Application  

APPLICANT: PXE International, Inc.

APPLICANT: Diversity of Hawaii

TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing;
TITLE OF INVENTION: Pseudoxanthoma Elasticum

TITLE OF INVENTION: UMBER: US/09/792,616

CURRENT APPLICATION UMBER: US/09/792,616

CURRENT FILING DATE: 2001-02-23

NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-071-035-408

Sequence 408, Application US/09071035

Patent No. 6448043

Patent No. 6448043

PAPLICANT: Gil H. Choi

TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
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                                                                                          Length 1498;
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                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                          Score 42; DB 4;
Pred. No. 5.2e+02;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 4;
Pred. No. 5.2e+02;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
                                                                                          58.3%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.3%;
71.4%;
                                                               Query Match
Best Local Similarity 71.**,
Best Local Similarity 71.**,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 58.3
Best Local Similarity 71.4
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                     ; ORGANISM: Mus musculus
US-09-792-616-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                              990 GYWLSLW 966
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965 GYWLSLW 971
                                                                                                                                                                                    2 GYWLTIW 8
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1503
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-792-616-3
; TYPE: PRT
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                                                 Sequence 187, Application US/09325932A

Sequence 187, Application US/09325932A

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: Flinn, Barry
APPLICANT: Plinn, Barry
APPLICANT: Plinn, Barry
APPLICANT: Compositions affecting programmed cell
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant develc
FILE REFERENCE: 1029-06-04
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
CURRENT FILING DATE: 1999-06-04
SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 187

LENGTH: 161
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APPLICANT: PXE International, Inc.
APPLICANT: PXE International, Inc.
APPLICANT: PXE International, Inc.
APPLICANT: University of Hawaii
TITLE GAMP: University of Hawaii
TITLE OF INVENTION: Pseudoxanthoma Blasticum
TITLE OF INVENTION: Pseudoxanthoma Blasticum
TITLE OF INVENTION: Pseudoxanthoma Blasticum
CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 1498
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Sequence 46926, Application US/09270767

Sequence 46926, Application US/09270767

Sequence 46926, Application US/09270767

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:
FILE REPERENCE: File Reference: 7326-094

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 46926

LENGTH: 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 4; Length 273;
Pred. No. 1e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09792616
Patent No. 6780587
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Matches 6, Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Pinus radiata
US-09-325-932A-187
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                                          US-09-325-932A-187
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US-09-792-616-9
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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RESULT 13
US-09-071-035-406

i Sequence 406, Application US/09071035

j Sequence 406, Application US/09071035

j Retent No. 64440043

j GENERAL INFORMATION:

APPLICANT: Gil H. Choi

TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides

NUMBER OF SEQUENCES: 496

CORRESPONDENCE ADDRESS:

ADDRESSESE: Human Genome Sciences, Inc.

STREET: 9410 KeW West Avenue

CITY: Rockville

CITY: Rockville

STATE: Maryland

COUNTRY: USA

THE OF INVENTIONS

COUNTRY: USA

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Patent No. 6428967;
GENERAL INFORMATION:
APPLICANT: Herz.
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways;
FILE REFERENCE: UTSWO708
CURRENT APPLICATION NUMBER: US/08/562,737;
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132;
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 81
LENGTH: 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM:
SOFTWARE: AGCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DAIE.

CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 62.5
Matches 5; Conservative
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                                                                        200 CGAWLGIW 207
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-071-035-406
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Patent No. 6673910

GENERAL INFORMATION:
FILE DE INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: 2709.2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

LENGTH: 264
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 032796-032
CURRENT FILING DATE: 1998-08-13
FRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 3630
LENGTH: 229
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 56.9%; Score 41; DB 4; Length 222; Best Local Similarity 62.5%; Pred. No. 1.2e+02; Matches 5; Conservative 2; Mismatches 1; Indels
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Pred. No. 1.2e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3630, Application US/09134000C Patent No. 6617156
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 408:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
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; ORGANISM: Enterococcus faecalis
US-09-134-000C-3630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vuery match
Best Local Similarity 62.5%;
Matches 5; Conservative ;
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Best Local Similarity 75.0
Matches 6; Conservative
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; ORGANISM: M.catarrhalis
US-09-540-236-2978
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179 GTWITLWG 186
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) ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
is OTHER INFORMATION: Sequence
US-09-562-737-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-562-737-87
                                                                                                                                Query Match 56.2%; Score 40.5; DB 4; Length 1024; Best Local Similarity 54.5%; Pred. No. 5.8e+02; Matches % 6; Conservative 2; Mismatches 2; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 56.2%; Score 40.5; DB 4; Length 1024; Best Local Similarity '54.5%; Pred. No. 5.8e+02; Matches 6; Conservative 2; Mismatches 2; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                  Sequence 87, Application US/09562737

Sequence 87, Application US/09562737

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Herz, Joachim
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: USW0708

CURRENT FILING DATE: 2000-05-01

WUMBER OF SEQ ID NOS: 132

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 87

LENGTH 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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892 CGEWIGTMWDC 902
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892 CGEWIETMWDC 902
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US-09-562-737-87
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Search completed: December 30, 2004, 13:19:20 Job time : 24.0189 secs

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December 30, 2004, 13:08:04 ; Search time 74.5283 Seconds (without alignments) 48.267 Million cell updates/sec
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(ganz 6/ptodata/1/pubpaa/US08 NEW PUB. DED: *

(ganz 6/ptodata/1/pubpaa/US08 NEW PUB. DED: *

(ganz 6/ptodata/1/pubpaa/US08 PUBCOMB. DED: *

(ganz 6/ptodata/1/pubpaa/US09 PUBCOMB. DED: *

(ganz 6/ptodata/1/pubpaa/US09 NEW PUB. DED: *

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Compugen Ltd.
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GenCore version
Copyright (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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72
1 CGYWLTIWGC 10
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 35, Appl	Sequence 34, Appl	Sequence 73, Appl	Sequence 2288, Ap	Sequence 1934, Ap	Sequence 476, App	Sequence 125253,	Sequence 54, Appl	Sequence 278, App	Sequence 743, App	Sequence 77862, A	Sequence 84, Appl	Semience 181150
SUMMARIES	ID	US-10-046-922-35	US-10-046-922-34	US-10-046-922-73	US-10-017-161-2288	US-10-292-798-1934	US-10-280-066-476	US-10-437-963-125253	US-10-125-869A-54	US-10-462-262-278	US-10-112-944-743	US-10-282-122A-77862	US-10-211-962-84	US-10-437-963-181150
		13	13	13	14	14	14	16	14	15	15	15	14	
	Query Match Length DB	10	10	10	304	304	25	63	17	17	136	828	1024	103
de ,	Ouery Match	100.0	75.0	69.4	0.99	66.0	65.3	65.3	63.9	63.9	63.9	62.5	61.8	61.1
	Score	72	24	50	47.5	47.5	47	47	46	46	46	45	44.5	44
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	7, 313	Sequence 7816, Ap		Sequence 57928, A	Sequence 190740,	1533,	2457,	1534,	2376,	13	10, Ap	86		1.,	w	_	Ů.	٠,	Seguence 3, Appli	٠,	••	119, 7		Sequence 338, App	43458,	a)	e 20464	e 24089	Sequence 332065,
-10-767-7	10-369- 10-369-	10-032-	10-437-	10-282-122A-5	10-437-963-19	19-833-245-1	0-264-237-24	9-833-245-153	0-276-774-23	33	0-161-927-1	0-211	0-388-470-	Ŧ	-09-864-408A-	-10-219-220-18	09-792-616-	10-764-328-	US-09-792-616-3	-10-764-328-	-10-108-260A-2	-493-	-125-869A-1	3-10-462-262-33	US-09-864-761-43458	3-10-424-59	-10-425-115	-10-424-599-240	US-10-425-115-332065
14	14	14	16	15	16	11	15	7	15	15	14	14	14	14	11	14	10	16	10	16	15	14	14	15	σ	15	17	15	17
161	13 291	454	459	474	671	152	152	159	161	161	176	1024	1765	1765	9	161	1498	1498	1503	1503	122	620	14	14	34	57	78	82	104
61.1 59.7	59.7	59.7	59.7	59.7	59.7	59.0	59.0	59.0	59.0	59.0	59.0	59.0	59.0	59.0	58.3	58.3		58.3	58.3	58.3	57.6	57.6	56.9	56.9	56.9	56.9	56.9	56.9	56.9
444	4 4 5 60	43	43	43	43	42.5	42.5	42.5	42.5	42.5	42.5	42.5	42.5	42.5	42	42	42	42	42	42	Ξ.	41.5	41	41	41	41	41	41	41
11.	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

US-10-046-922-35

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Gaps
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Sequence 35, Application US/10046922

Publication No. US20020164667A1

GENERAL INFORMATION:

APPLICANT: Alitalo, Kari

APPLICANT: Koivunen, Erkki

APPLICANT: Koivunen, Erkki

TITLE OF INVENTION: WEGRE-3 INHIBITOR MATERIALS AND METHODS

FILE REFERENCE: 28967/37084A

CURRENT FILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 80

SOFTWARET Extentin version 3.0

SEQ ID NO 35

LENGTH: 10
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100.0%; Pred. No. 0.0026;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 34, Application US/10046922; Publication No. US20020164667A1; GENERAL INFORMATION: APPLICANT: Alitalo, Kari; APPLICANT: Koivunen, Erkki
                                                                                                                                                                                                                                                                                         TYPE: PRT ; ORGANISM: isolated peptide US-10-046-922-35
                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 10; Conservative
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US-10-046-922-34
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APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REPERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FLING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR RILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 2288
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MOD RES
LOCATION: (79)...(83)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Variable amino acid
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OTHER INFORMATION: Variable amino acid
FEATURE:
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LOCATION: (118)..(119)
OTHER INFORMATION: Variable amino acid
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OTHER INFORMATION: Variable amino acid
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OTHER INFORMATION: Variable amino acid
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LOCATION: (219)
OTHER INFORMATION: Variable amino acid
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OTHER INFORMATION: Variable amino acid
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OTHER INFORMATION: Variable amino acid
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LOCATION: (107)
OTHER INFORMATION: Variable amino
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OTHER INFORMATION: Variable amino
                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MOD RES
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LOCATION: (85)
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LOCATION: (123)
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NAME/KEY: MOD_RES
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NAME/KEY: MOD_RES
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Sequence 73, Application US/10046922

Publication No. US20020164667A1

GENERAL INFORMATION:

APPLICANT: Alitalo, Kari

APPLICANT: Kubo, Hajime

TILLE OF INVENTION: VEGRR-3 INHIBITOR MATERIALS AND METHODS

FILE REPERENCE: 28967/37084A

CURRENT FILING DATE: 2002-01-15

CURRENT FILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 80

SEQ ID NO 73

LENGTH: 10

MANARAMETER PATENTIN VERSION 3.0

SEQ ID NO 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.4%; Score 50; DB 13; Length 10; 60.0%; Pred. No. 2.5; 4; Indels tive 0; Mismatches 4; Indels
       APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 2896/737084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 34
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 75.0%; Score 54; DB 13; Length 10; Best Local Similarity 100.0%; Pred. No. 0.72; Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                               PEATURE:
| NAME/KEY: SITE
| LOCATION: (1)..(1)
| OTHER INFORMATION: X is any amino acid
| NAME/KEY: SITE
| LOCATION: (10)..(10)
| OTHER INFORMATION: X is any amino acid
| US-10-046-922-34
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OTHER INFORMATION: X is any amino acid
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; LOCATION: (9)...(9)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60.0.
                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: isolated peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: peptide library
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US-10-046-922-73
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OTHER INFORMATION: Variable amino acid
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MISC FEATURE; OTHER INFORMATION: Tiel-20C-3-D116
US-10-280-066-476
                                                                                                                                                                                                                                                                                                                                                                                                     66.0%;
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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ORGANISM: Eschericia coli
FEATURE:
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Sequence 1394, Application US/10292798

Publication No. US2003235833A1

GENERAL INFORMATION:

APPLICANT: SUMA, MAKIKO

APPLICANT: ARIYAMA, YUTAKA

APPLICANT: ARIYAMA, YUTAKA

TITLE OF INVENTION: GLANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS

FILE REFERENCE: 084335/16

CURRENT PELICATION NUMBER: US/10/292,798

CURRENT PILING DATE: 2002-11-13

PRIOR APPLICATION NUMBER: 10/017,161

PRIOR FILING DATE: 2001-06-18

PRIOR FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2070

SOFTWARE: PatentIN Ver: 2.1

SEQ ID NO 1334
                                                                                                                                                                          Gaps
                                                                                                                           Query Match 66.0%; Score 47.5; DB 14; Length 304; Best Local Similarity 60.0%; Pred. No. 88; Astches 6; Conservative 2; Mismatches 1; Indels 1.
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (256)..(289)
; OTHER INFORMATION: Variable amino acid
US-10-017-161-2288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MOD RES
LOCATION: (73\)..(73)
OTHER INFORMATION: Variable amino acid
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OTHER INFORMATION: Variable amino acid
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LOCATION: (897...(91)
OTHER INFORMATION: Variable amino acid
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NAME/KEY: MOD RES
LOCATION: (96)..(97)
OTHER INFORMATION: Variable amino acid
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OTHER INFORMATION: Variable amino acid
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NAME/KEY: MOD RES
LOCATION: (107)..(107)
OTHER INFORMATION: Variable amino acid
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LOCATION: (118)..(119)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MOD RES
LOCATION: (121)..(121)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                   108 CGFW-AVWGC 116
                                                                                                                                                                                                             1 CGYWLTIWGC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MOD_RES
LOCATION: (123)..(123)
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LOCATION: (80)..(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                      US-10-292-798-1934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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us-tu-280-066-476
; Sequence 476, Application US/10280066
; Publication No. US20030180718A1
GENERAL INFORMATION:
    APPLICANT: Pillutla, Renuka C.
    APPLICANT: Pillutla, Renuka C.
    APPLICANT: Bridette, Renee
    APPLICANT: Bridette, Renee
    APPLICANT: Blume, Arthur J.
    APPLICANT: Prendergast, John
    APPLICANT: Prendergast, John
    APPLICANT: Goldstein, Neil I.
    TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BIND
    FILE REFERENCE: 2598-4009US1
    CURRENT APPLICATION NUMBER: US/10/280, 066
    CURRENT APPLICATION NUMBER: 60/345,471
    PRIOR FILING DATE: 2001-10-24
    NUMBER OF SEQ ID NOS: 537
    SOFTWARE: Patentin version 3.1
    SEQ ID NO 476
    LENGTH: 25
    FILE APPLICATION NUMBER: DATE SECOND SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 304;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IndelB
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Pred. No. 88;
2; Mismatches
                                                                                                                                                                              PEATURE:
NAME/KEY: MOD_RES
LOCATION: (210)..(211)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:

NAME/KEY: MOD RES

LOCATION: (256)..(289)

CHER INFORMATION: Variable amino acid

15-10-29-798-1934
FEATURE:
NAME/KEY: MOD RES
LOCATION: (178) ..(178)
OTHER INFORMATION: Variable amino acid
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LOCATION: (219)...(219)
OTHER INFORMATION: Variable amino acid
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEX: misc_feature
LOCATION: (1)...(136)
OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set fort
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                           63.9%; Score 46; DB 15; Length 17; 66.7%; Pred. No. 13; 2; Indels tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ghosh, Malabika
APPLICANT: Wang, Dunrui
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Zhiwei
TITLE OF INVENTION: No. US20040048249Alel Nucleic Acids and
TITLE OF INVENTION: Secreted Polypeptides
                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: immunoglobulin binding polypeptide US-10-462-262-278
         FILE REFERENCE: 10280-052001
CURRENT APPLICATION NUMBER: US/10/462,262
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: US 60/388,642
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 430
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 278
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR PRILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-13
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 924
SOFTWARE: PL_Genes Version 5.0
LENGTH: 136
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CURRENT APPLICATION NUMBER: US/10/112,944
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 09/488,725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 743, Application US/10112944
Publication No. US20040048249A1
GENERAL INFORMATION:
  TITLE OF INVENTION: PROTEIN ANALYSIS
                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tang, Y. Tom
APPLICANT: Yang, Yonghong
APPLICANT: Weng, Gezhi
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Xue, Aidong J.
APPLICANT: Weng, Jian-Rui
APPLICANT: Wehrman, Tom
                                                                                                                                                                                                                                                                                                                                                                              Query Match 63.9
Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CGYWLTIWG 9
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US-10-112-944-743
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                                                          APPLICANT: Boukharov, Andrey A. APPLICANT: Boukharov, Andrey A. APPLICANT: Barbazuk, Brad APPLICANT: Barbazuk, Brad APPLICANT: Barbazuk, Brad APPLICANT: Li, Ping APPLICANT: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5321)8 CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 125253 LENGTH: 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.9%; Score 46; DB 14; Length 17; 66.7%; Pred. No. 13; 2; Indels tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 54, Application US/10125869A

Sequence 54, Application No. US20030199671A1

GENERAL INCORMATION:

APPLICANT: Rondon, Isaac Jesus

APPLICANT: W. Q.'Long

APPLICANT: Bey, Arthur C.

APPLICANT: Stochl Mark

APPLICANT: Stochl Mark

TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION

TITLE OF INVENTION: PONYEPTIDES

FILE REFERENCE: 3421.1006-001

CURRENT PILING DATE: 2002-11-19

FRIOR FILING DATE: 2001-04-18

NUMBER: OF SEQ ID NOS: 200

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 54

LENGTH. 17
                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT4530_27915C.1.pep
US-10-437-963-125253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: Fc region binding polypeptide
US-10-125-869A-54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.0
Matches 6; Conservative
Zhou, Yihua
Cao, Yongwei
Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CGYWLTIWGC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 CGHYLKAWGC 46
                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGYWLTIWG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-462-262-278
                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
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Sequence 84, Application US/10211962
Publication No. US20030082640A1
GENERAL INFORMATION:
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Best Local Similarity 54.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 892 CCHWIETMWDC 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CGYWL-TIWGC 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 YWLTIWGC 10
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19 WWVSVWGC 26
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Best Local Similarity
Matches 4; Conserv
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## TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

## CURRENT APPLICATION NUMBER: US/10/282,122A

## CURRENT FILING DATE: 2003-02-20

## PRIOR APPLICATION NUMBER: 60/201,078

## PRIOR APPLICATION NUMBER: 60/206,848

## PRIOR APPLICATION NUMBER: 60/206,848

## PRIOR FILING DATE: 2000-05-23

## PRIOR FILING DATE: 2000-05-24

## PRIOR FILING DATE: 2000-05-06

## PRIOR FILING DATE: 2000-09-06

## PRIOR FILING DATE: 2000-10-23

## PRIOR FILING DATE: 2000-11-27

## PRIOR FILING DATE: 2000-10-2-09

## PRIOR FILING DATE: 2000-10-2-09

## PRIOR FILING DATE: 2001-02-09

## PRIOR FILING DATE: 2001-02-09

## PRIOR PILING DATE: 2001-02-09

## PRIOR APPLICATION NUMBER: 60/267,636

## PRIOR PILING DATE: 2001-02-09

## PRIOR PILING DATE: 2001-02-0
                                                                                                                                                                Gaps
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                                                                                           Score 46; DB 15; Length 136;
Pred. No. 73;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 828;
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Pred. No. 4.3e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 77862, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
; OTHER INFORMATION: in Example 2 US-10-112-944-743
                                                                                           63.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                     Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 ĆĠĿŴĹELLSŴĠĊ 383
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; ORGANISM: Yersinia pestis
US-10-282-122A-77862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CGYWLTI--WGC 10
                                                                                                                                                                                                                                                                  93 CGRWDWLWGC 102
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RESULT 12 US-10-211-962-84

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APPLICANT: Li, Ping,
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 181150
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                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; JOTHER INFORMATION: Sequence
US-10-211-962-84
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Pred. No. 6e+02;
3; Mismatches 1; Indels 1;
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APPLICANT: Getthardt, Michael
APPLICANT: Gotthardt, Michael
TILE OF INVENTION: LDL Receptor Signaling Pathways
FILE REPERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/10/211,962
CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US/09/562,737
PRIOR APPLICATION OF 132
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT4530_78451C.1.pep
US-10-437-963-181150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.1%; Score 44; DB 16; I
llarity 50.0%; Pred. No. 1.1e+02;
Conservative 4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 181150, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-767-701-54778; Application US/10767701; Sequence 54778; Application Ws/10767701; Publication No. US20040172684A1; GENERAL INFORMATION: APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.8%;
54.5%;
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 54778
LENGTH: 161
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                                                                                                                                                                                                                   Query Match 61.1%; Score 44, DB 16; Length 161;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Fc region binding polypeptide US-10-125-869A-73
                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: 14593586.pep
US-10-767-701-54778
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ORGANISM: Artificial Sequence
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Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                       TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
                                                                                                                                                                                                                                                                                            150 CGYWLKPW 157
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

December 30, 2004, 12:58:17 ; Search time 11.5094 Seconds (without alignments) 83.598 Million cell updates/sec Run on:

US-10-046-922-35 1 CGYWLTIWGC 10 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### STIMMADIES

	Description	hypothetical prote	₩	_	sodium channel alp	proteir	probable transport	multidrug resistan	oxaloacetate decar	hypothetical prote	replication protei	permease [imported	hypothetical prote	sodium channel alp	channel		sodium channel pro	channel	channel	sodium channel alp	channel	channel	channel	channel	sodium channel alp	sodium channel pro	Bodium channel alp	channel	sodium channel pro	sodium channel pro
SUMMARIES	ΩI	S76385	AD0412	T30902	T42388	230980	C95307	T42216	F70439	T48166	411	E90446	T29407	148108	A55138	A45380	CHEE	I54323	I64893	JS0648	I51964	CHRTM1	S00320	I56555	S54771	A60054	A46269	B25019	A25019	A38195
	DB	7	7	7	~	~	7	7	7	N	N	~	7	7	7	7	-	7	7	~	~	-	~	~	~	~	~	~	~	N
	Query Match Length	218		-	1765	72	441	1502	620	307	391	419	739	200	1681	1682	1820	1835	1836	1836	1836	1840	1951	1976	1977	1983	2002	00	8	5
d	Query Match	l M	62.5	0	59.0	58.3	58.3	58.3	57.6	56.9	56.9	56.9	56.9	56.2	56.2	56.2	56.2	56.2	56.2	56.2	26.2	56.2	56.2	56.2	26.2	56.2	56.2	56.2	56.2	56.2
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sodium channel pro	sodium channel pro	Ig heavy chain pre	phenylalanyl-tRNA	probable ABC trans	probable Na+/H+-ex	probable ABC trans	genome polyprotein	probable aldo/keto	D-amino-acid oxida	D-amino-acid oxida	D-amino-acid oxida	D-amino-acid oxida	hypothetical prote	neurexin III beta	neurexin III beta
A33996	T43161	C34903	F97190	F95406	B71038	C95282	S64740	AH0289	JH0185	OXPGDA	S01340	JX0132	AF1978	A53580	B53580
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019	2049	142	339	359	425	508	2344	298	345	347	347	347	376	392	426
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56.2 2	56.2	55.6	55.6	55.6	55.6	55.6	55.6	54.9	54.9	54.9	54.9	54.9	54.2	54.2	54.2
40.5 56.2 2				40 55.6						39.5 54.9					

### ALIGNMENTS

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hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
C;Species: So-Apr-1997 #text_change 09-Jul-2004
C;Accession: S76385
C;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Accession: $76385
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-218 <KAN>
A,Cross-references: UNIPROT:Q55705, EMBL:D64000, GB:AB001339; NID:g1001484; PIDN:BAA1023
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C,Superfamily: probable alkaline phosphatase yngC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S74322; MUID: 97061201; PMID: 8905231
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Length 218; Query Match

Gaps ö 2; Indels 63.9%; Score 46; DB 2; 66.7%; Pred. No. 8.1; tive 1; Mismatches 6; Conservative Best_Local_Similarity Matches 6; Conserv

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CGYWVGRWG 81 1 CGYWLTIWG 9 73 ઠે g

ATP-dependent helicase [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004 C;Accession: AD0412 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. R;Parkhill, J.; Wren, B.W.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; J., M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001

A,Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A,Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AD0412

A;Equal: preliminary

A;Molecule type: DNA

A;Residues: 1-828 <KUR>
A;Residues: UNIPROT:Q82BL4; GB:AL590842; PIDN:CAC92624.1; PID:g15981320; GSPDB:C C; Genetics:

A;Gene: hrpB C;Superfamily: ATP-dependent RNA helicase, HrpB type

62.5%; Score 45; DB 2; Length 828; Query Match

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A;Status: nucleic acid sequence not shown; translation not shown
A;Nolecule type: DNA
A;Residues: 1-72 < DDNA
A;Residues: 1-72 < DDNA
A;Residues: 1-72 < DDNA
A;Residues: 1-72 < DDNA
A;Cross-references: UNIPROT:Q05245; EMBL:Z18946; NID:g15859; PIDN:CAA79411.1; PID:g15891
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
C;Genetics:
A;Gene: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: C95307
R; Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse R; Barnett, M.J.; Fisher, R.F.; Jones, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C., Froc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A; Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilots A; Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-441 cKUR>
A; Residues: 1-441 cKUR>
A; Cross-references: UNIPROT: Q922T6; GB: Ab006469; PIDN: AAK65021.1; PID: G14523451; GSPDB: GR
A; Cross-references: UNIPROT: Q922T6; GB: Ab006469; PIDN: AAb012, P: Ampe, F: Barloy-Hubler, R: A; Experimental source: strain 1021, megaplasmid pSymA
R; Galibert, F:; Finan, T.W.; Long, S.R.; Puhlar, A.; Abola, P:; Ampe, F:; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandembol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.Cl A; Reference number: Aselogome of the legume symbiont Sinorhizobium meliloti.
A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: T42216
R;Hirohashi, T.; Suzuki, H.; Ito, K.; Ogawa, K.; Kume, K.; Shimizu, T.; Sugiyama, Y.
Mol. Pharmacol. 53, 1068-1075, 1998
A;Title: Hepatic expression of multidrug resistance-associated protein-like proteins main A;Reference number: Z22081; MUID:98279126; PMID:9614210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1502 <HIR>
A;Kesidues: 1-1502 <HIR>
A;Cross=references: UNIRROT:088269; EMBL:AB010466; NID:g3242457; PIDN:BAA28954.1; PID:g32
A;Experimental source: strain Sprague-Dawley; liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable transport protein SMa0684 [imported] - Sinorhizobium meliloti (strain 1021) maga
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C.Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                    Length 72
                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                    Score 42; DB 2
Pred. No. 12;
1; Mismatches
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Pred. No. 58;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: L-lysine transport protein
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71.4%;
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Best Local Similarity
Matches 5; Conserv
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A,Gene: SMa0684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42389
R;Dib-Haji, S.D.; Tyrrell, L.; Black, J.A.; Waxman, S.G.
Proc. Natl. Acad. Sci. U.S.A. 95, 8961-8968, 1998
A;Title: NaN, a novel voltage-gated Na channel, is expressed preferentially in periphera A;Reference number: Z22149; MUID:98338024; PMID:9671787
A;Accession: T42388
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Species: Mycobacterium phage L5
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: 830980
R;Donnelly-Wu, M.K.; Jacobs Jr., W.R.; Hatfull, G.F.
A)- Microbiol. 7, 407-417, 1993
A;Title: Superinfection immunity of mycobacteriophage L5: applications for genetic trans
A;Reference number: 830949; MUID:93211283; PMID:8459767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Residues: 1-1765 <DIB>
A,Residues: 1-1765 <DIB>
A,Zross-references: UNIPROT:088457; EMBL:AF059030; NID:g3372614; PID:g3372615; PIDN:AAC4
A,Experimental source: strain Sprague-Dawley; dorsal root ganglia
A,Note: preferentially expressed in sensory neurons within dorsal root ganglia and trige
                                                                                                                                                                                                                                                                                                                                        C;Species: Aplysia californica (California aca hare)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30902
R;Dyer, Johnston, W.L.; Castellucci, V.F.; Dunn, R.J.
DNA Cell Biol. 16, 347-356, 1997
A;Title: Cloning and tissue distribution of the Aplysia Na+ channel alpha-subunit CDNA. A;Reference number: Z20329, MUID:97238630; PMID:9115644
A;Accession: T30902
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P90670; EMBL:U66915; NID:g1842248; PID:g1842249; PIDN:AAC474
C;Superfamily: sodium channel protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 60.4%; Score 43.5; DB 2; Length 1993; Local Similarity 54.5%; Pred. No. 1.3e+02; les 6; Conservative 3; Mismatches 1; Indels 1
                                   Indels
                                                                                                                                                                                                                                                                                                                           sodium channel SCAP1 alpha chain - California sea hare
                                   5
      Pred. No. 36;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: sodium channel protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sodium channel alpha chain - rat
                                                                                                                                                        372 CGLWLELLSWGC 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 54.5
      Similarity 58.77, Conservative
                                                                                                 1 CGYWLTI--WGC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            || |: ::|||
CGEWIESMWGC 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || |: :|||
CGEWIENMWGC 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CGYWL-TIWGC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CGYWL-TIWGC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Residues: 1-1993 <DYE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S30980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            942
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      Best Local
Matches
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Matches
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Derméase [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 2-4May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: E50446
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrett, R.A.; Sangan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q97VB7; GB:AE006641; NID:g13816037; PIDN:AAK42828.1; GSPDB:G
C;Genetics:
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A;Introns: 68/2; 179/3; 253/1; 275/3; 327/2; 365/3; 397/1; 428/2; 463/3; 629/1; 668/2; 7
                    replication protein homolog - Pyrococcus sp. (fragment)
N,Alternate names: hypothetical 391 protein
C;Species: Pyrococcus sp.
C;Species: V7-Peb-1996 #sequence_revision 19-Apr-1996 #text_change 17-May-1996
C;Accession: PC4117
R;Rashid, N.; Morikawa, M.; Imanaka, T.
Gene 166, 139-143, 1995
A;Title: An abnormally acidic TATA-binding protein from a hyperthermophilic archaeon. A;Reference number: JC4514; MUID:96102215; PMID:8529878
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A;Cross-references: EMBL:U80452; PIDN:AAB37863.1; GSPDB:GN00020; CESP:C16C8.2
A;Experimental source: strain Bristol N2; clone C16C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hyporhetical protein C16C8.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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R;Waterston, R.; Le, T.T.; Gattung, S.
submitted to the EMBL Data Library, November 1996
A;Description: The sequence of C. elegans cosmid C16C8.
A;Accession: T29407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule,type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 2;
Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB
Pred. No. 78;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.9%;
62.5%;
                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-391 <RAS>
A;Cross-references: DDBJ:D50018
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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365 GFWETLWG 372
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Beet Local Similarity
5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-419 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GYWLTIWG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: E90446
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R; Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov V. S. Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov V. Nature 392, 353-358, 1998
A; Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A; Reference number: A70300; MUID:98196666; PMID:9537320
A; Accession: F70439
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Resperimental source: strain VF5
A; Cross-references: UNIPROT:067544; GB:AE000747; NID:g2983944; PIDN:AAC07497.1; PID:g298
A; Experimental source: strain VF5
C; Genetics:
A; Gene: oadA
C; Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/biot
F; 540-613/Domain: lipoyl/biotin-binding homology < LPB>
F; 579/Binding site: biotin (Lys) (covalent) #status predicted
C; Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein T1008.150 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48166
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer, is submitted to the Protein Sequence Database, March 2000
A;Reference number: 224486
A;Accession: T48166
A;Accession: T48166
A;Accession: T4816
A;Accession: T4816
A;Accidues: DNA
A;Residues: J-307 4EBV>
A;Cross-references: UNIPROT:Q9M030; EMBL:AL161746
A;Experimental source: cultivar Columbia; BAC clone T1008
C;Genetics:
A;Map position: 5
A;Introns: 31/3; 66/2; 114/3; 149/2; 232/2; 284/1
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                                                                                                                                                                                                                                                                                                                                                                                                       Species: Aquifex aeolicus
:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
:Accession: F70439
                                                                                                                       Gaps
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                                                        Query Match 58.3%; Score 42; DB 2; Length 1502; Best Local Similarity 71.4%; Pred. No. 1.7e+02; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.9%; Score 41; DB 2; Length 307; 50.0%; Pred. No. 60;
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                                                                                                                                                                                                                                                                                                                                                                             oxaloacetate decarboxylase alpha chain - Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
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964 GYWLSLW 970
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Matches 5; Conserv
                                                                                                                                                                          2 GYWLTIW 8
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                                                                                                                                                                                                                                                                                                                                       odium channel alpha subunit - long-tailed hamster (fragment)
C;Species: Cricetulus longicaudatus (long-tailed hamster)
C;Species: Cricetulus longicaudatus (long-tailed hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 148108
R;Lalik, P.H.; Krafte, D.S.; Ciccarelli, R.B.
A;Title: Characterization of endogenous Sodium channel gene expressed in chinese hamster
A;Reference number: 148108
A;Accession: 148108
A;Accession: I48108
A;Residues preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-200 <RES>
A;Cross-references: UNIPROT:Q60464; GB:M87541; NID:g191069; PIDN:AAA36979.1; PID:g553840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sodium channel mNa2.3, voltage-gated - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: A55138
R;Felipe, A.; Knittle, T.J.; Doyle, K.L.; Tamkun, M.M.
J. Biol. Chem. 269, 30125-30131, 1994
A;Title: Primary structure and differential expression during development and pregnancy
A;Reference number: A55138, MUID:95074002; PMID:7982916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A)Reaidues: 1-1681 <FEL>
A)Cross-references: UNIPROT:Q62467; GB:L36179; NID:g609544; PIDN:AAA66192.1; PID:g806397
C;Superfamily: sodium channel protein
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sodium channel protein alpha chain hNav2.1 - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A45380
R;George Jr., A.L.; Knittle, T.J.; Tamkun, M.M.
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.2%; Score 40.5; DB 2; Length 200; 54.5%; Pred. No. 49; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
                                            56.9%; Score 41; DB 2; Length 739; 60.0%; Pred. No. 1.3e+02; tive 1; Mismatches 3; Indels
C;Superfamily: myeloperoxidase; myeloperoxidase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: chol
C;Superfamily: sodium channel protein
C;Keywords: duplication
                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 54.5
Matches 6; Conservative
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CGEWIETMWDC 36
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                                                                                                                                                                                          118 CGFWATIREC 127
                                                                                                                                                           1 CGYWLTIWGC 10
                                                                           Best Local Similarity
                                                    Query Match
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Proc. Natl. Acad. Sci. U.S.A. 89, 4893-4897, 1992
A;Title: Molecular cloning of an atypical voltage-gated sodium channel expressed in human A;Reference number: A45380; MUID:92279233; PMID:1317577
A;Accession: A45380
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1682 <GGD>A;Cross-references: UNIPROT:Q01118; GB:M91556; NID:G189046; PIDN:AA59899.1; PID:G189047
A;Cross-references: UNIPROT:Q0118; GB:M91556; NID:G189046; PIDN:AA59899.1; PID:G189047
A;Cross-references: UNIPROT:Q0118; GB:M9156; NID:G189046; PIDN:AA59899.1; PID:G189047
A;Cross-references: UNIPROT:Q0118; PID:G189046; PIDN:AA59899.1; PID:G189047
A;Cross-references: UNIPROT:Q0118; PID:G189046; PIDN:AA59899.1; PID:G189047
A;Cross-references: UNIPROT:Q0118; PID:G189046; PID:G189046; PID:G189046; PID:G189046; PID:G189046; PID:G189046; PID:G189047
A;Cross-references: UNIPROT:Q0118; PID:G189046; PID:G189046; PID:G189046; PID:G189047
A;Cross-references: UNIPROT:Q01189046; PID:G189046; PID:G189046; PID:G189047
A;Cross-references: UNIPROT:Q01189046; PID:G189046; PID:G189047
A;Cross-references: UNIPROT:Q0189046; PID:G189046; PID:G189
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GenCore version 5.1.6
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OM protein - protein search, using sw model Run on:

December 30, 2004, 12:57:52 ; Search time 92.2641 Seconds (without alignments) 62.362 Million cell updates/sec

US-10-046-922-35 72 1 CGYWLTIWGC 10

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	2000		Q8zbl4 yersinia pe		66 yersini	P90670 aplysia cal				Q6c574 yarrowia li	Q8dkd6 synechococc	Q8h2n7 oryza sativ	Q7wy20 pseudomonas		homo	Q9nrw9 homo sapien	Q96pl4 homo sapien	56 hor	Q7yyfl cryptospori		Q05245 mycobacteri		Q6mc01 parachlamyd	9	Q94fs2 cajanus caj	Q83151 tropheryma			~	G		. ,
SUMMAKIES	Ę	Y232_SYNY3	Q8ZBL4	Q8D1A7	AAS60566	P90670	Ф6н022	Q74JK6	AAS08923	Q6C574	QBDKD6	Q8H2N7	Q7WY20	Q96AC0	QGRW13	Q9NRW9	Q96PL4	AAR25556	Q7YYF1	088457	VG35 BPML5	Q855 <u>1</u> 3	Q6MC01	CAF23898	Q94FS2	083151	Q92ZT6	Q83G14	RBL NITVU	09x <u>0</u> 76	09XD77	
	ä	-		0	0	~	7	7	7	N	7	7	N	7	7	7	~	7	7	7	-1	7	~	7	7	7	7	0	-1	7	7	•
	Query Match Length	218	828	853	853	1993	168	221	221	501	646	733	1084	152	159	159	159	159	263	1765	72	133	284	284	343	389	441	452	472	473	473	
	Query			62.5	62.5	60.4	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.0	59.0	59.0	59.0	59.0	59.0	59.0	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	- (
	er co	46	45	45	45	43.5	43	43	43	43	43	43	43	42.5	42.5	42.5	42.5	42.5	42.5	•	42	42	42	42	42	42	42	42	42	42	42	•
	Result	-	01	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	56	27	28	59	30	ř

RESULT 2
Q8ZBL4
D Q8ZBL4
AC Q8ZBL4;
D 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

||||: || CGYWVGRWG 81 1 CGYWLTIWG 9

73

ð 요

Q8t6h2 dictyosteli		O88269 rattus norv		O8n1z5 homo sapien	067544 aquifex aeo	082z85 enterococcu	Q9m030 arabidopsis		Q8iud8 homo sapien		Q97vb7 sulfolobus	Office Office	Aah59368 homo sapi
О8Т6Н2	MRP6_MOUSE	MRP6 RAT	MRP6 HUMAN	Q8N1 <u>Z</u> 5	067544	082285	Q9M030	Q6CBE4	Q81UD8	Q9HKA9	Q97VB7	OGNURO	AAH59368
~		Н	7	~	7	7	~	~	~	~	~	~	0
1308	1498	1502	1503	122	620	266	307	376	398	413	419	432	432
58.3	58.3	58.3	58.3	57.6	57.6	56.9	56.9	56.9	56.9	56.9	56.9	56.9	56.9
42	42	42	42	41.5	41.5	41	41	41	41	41	41	41	41
32	33	34	32	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1

Y232	
AC	
5	01-NOV-1997 (Rel. 35, Created)
4 5	
DE	Hypothetical protein glr0232.
S	OrderedLocusNames=s1r0232;
SO	Synechocystis sp. (strain PCC 6803).
႘	Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
ŏ	NCBI_TaxID=1148;
RN	[1] _
RP	SEQUENCE FROM N.A.
Σ	MEDLINE=96127529; PubMed=8590279;
æ	Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA.	Sugiura M., Tabata S.;
RŢ	"Sequence analysis of the genome of the unicellular cyanobacterium
RŢ	Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT	region from map positions 64% to 92% of the genome.";
RI.	DNA Res. 2:153-166(1995).
႘	-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
႘	-!- SIMILARITY: Belongs to the deda family.
႘	
ပ္ပ	This SWISS-PROT entry is copyright. It is produced through a collaboration
ပ္ပ	between the Swiss Institute of Bioinformatics and the EMBL outstation -
႘	the European Bioinformatics Institute. There are no restrictions on its
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႘	or send an email to license@isb-sib.ch).
ပ္ပ	
DR DR	EMBL; D64000; BAA10237.1;
DR	PIR; S76385; S76385.
띪	InterPro; IPR000252; DedA.
띪	Pfam; PF00597; DedA; 1.
Æ	Complete proteome; Hypothetical protein.
SO	SEQUENCE 218 AA; 23781 MW; C04B5D7B7EA7F863 CRC64;
ಕ.	63.9%;
ž ž	Concompation 1 Minorabot 2 Teals 0 Gene
) 	of conservative if mismacches 2;

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Bacteriol. 184:4601-4611(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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AAS60566
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STRAIN=KIMS / Biovar Mediaevalis;
STRAIN=KIMS / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
Perry R.D.;
"Genome sequence of Versinia pestis KIM.";
                                                                                                           SEQUENCE FROM N.A.
STRAIN=CO-92 / Biovar Orientalis;
STRAIN=CO-92 / Biovar Orientalis;
MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L., Baker S., Bacham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Mature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yersinia pestis.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
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                                                                                                                                                                                                                                                                                       FIRE, AD0412; AD0412.

QC; GO:0005524; F:ATP binding; IEA.

QC; GO:0008026; F:ATP-dependent healicase activity; IEA.

QC; GO:0008026; F:ATP-dependent healicase activity; IEA.

QC; GO:0008076; F:Mydrolase activity; IEA.

QC; GO:0003676; F:Mydrolase activity; IEA.

RITHERPO: IPRO01410; DEAD.

RITHERPO: IPRO10225; DEAH DOX HTDB.

RITHERPO: IPRO10225; DEAH DOX HTDB.

RITHERPO: IPRO10259; Helicase_C.

RITHERPO: IPRO0271; Helicase_C.

REAM: PF00271; Helicase_C.

REAM: PF00271; Helicase_C.

REAM: SWART; SW00487; DEXDC; I.

REAM: SWART; SW00487; DEXDC; I.

REAM: TIGREAMS; TIGROLFO: DEAH DOX HTDB; 1.

REAM: TIGREAMS; TIGROLFO: I.

RATP-binding; COMPlete profeome; Helicase; Hydrolase.

SEQUENCE 828 AA; 91982 MW; 3A11F88835D55583 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.5%; Score 45; DB 2; Length 828; 58.3%; Pred. No. 2.4e+02; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8D1A7 PRELIMINARY; PRT; 853 AA. Q8D1A7; 074XU2; 01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2004 (TrEMBLrel. 28, Last annotation update) Helicase, ATP-dependent.
    01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=hrpB; OrderedLocusNames=YP0291, y0794;
                 ATP-dependent helicase.
Name=hrpB; OrderedLocusNames=YPO3394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372 CGLWLELLSWGC 383
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nes 7; Conservative
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                                               Yersinia pestis.
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                                                                                    NCBI_TaxID=632;
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SEQUENCE FROM N.A.
STRANTS-1001 / Biovar Mediaevalis;
SORGY Y. Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
Yang R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
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58.3%; Pred. No. 2.5e+02;
ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J.,
Yang R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                         EMBL; AE013681; AAM84381.1; -.
EMBL; AE017128; AAS60566.1; -.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000804386; F:ATP-dependent helicase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0005676; F:nucleic acid binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMAKT; SMU0490; HELLICC; 1.
TIGREMAS; TIGRO1970; DAM-DOX_HTDB; 1.
ATP-binding; Helicase; Hydrolase.
SEQUENCE 853 AA; 95004 MW; B3DB738A18665B42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    853 AA; 95004 MW; B3DB738A18665B42 CRC64;
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24-MAR-2004 (TrEMBLrel. 27, Created)
24-MAR-2004 (TrEMBLrel. 27, Last sequence update)
4-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Helicase, ATP-dependent.
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InterPro; IPR011545; DEAD/DEAH N.
InterPro; IPR0101225; DEAH/DOX_HrpB.
InterPro; IPR001502; Helicase_Gom.
Pfam; PF00270; DEAD; 1.
Pfam; PF00270; DEAD; 1.
Pfam; PF00470; Helicase_dom.
Pfam; PF00470; Helicase_dom.
Pfam; PF00470; Helicase_C; 1.
PIRSP; PIRSP00496; ATP_hel_hrpB; 1.
SWART; SW00487; DEADC; 1.
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SEQUENCE FROM N.A.
STRAIN=91001 / Biovar Mediaevalis;
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Best Local Similarity 58....
Best Local 7; Conservative
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nes 7; Conservative
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    J. Bacteriol. 186:4338-4349(2004).

                                                                                      SEQUENCE FROM N.A.
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PubMed=14966310;
                                                                                                               STRAIN=FD33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q74JK6;
05-JUL-2004
05-JUL-2004
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02-mar-2004
                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                               01-MAY.1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-2094 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Sodium channel alpha-subunit SCAPI.
Aplysia californica (California sea hare).
Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea; Aplysioidea; Aplysiidae, Aplysia.
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GO; GO:001518; C:voltage-gated sodium channel complex; IEA.

GO; GO:0005218; C:voltage-gated sodium channel complex; IEA.

GO; GO:0005248; P:voltage-gated sodium channel activity; IEA.

GO; GO:0006812; P:voltage-gated sodium channel activity; IEA.

GO; GO:0006812; P:voltage-gated sodium channel activity; IEA.

GO; GO:0006812; P:voltage-gated sodium channel activity; IEA.

R GO; GO:0006812; P:voltage-gated sodium channel activity; IEA.

R InterPro; IPR00111; Cat channel TrpL.

R InterPro; IPR005821; Ion_trans.

R InterPro; IPR005820; Ma-trans.

R InterPro; IPR001596; Na_trans.

R Pfam; PF06521; Ion_trans; 4.

R Pfam; PF06512; Na_trans assoc.

R Pfam; PF06512; Na_trans assoc.

R Pfam; PF06512; Na_trans assoc; 1.

R PRINTS; PR00110; Na_trans.

M Transport; Ionic channel; Sodium channel; Transmembrane;

M Transport; Voltage-gated channel.

Transport; Voltage-gated channel.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
4 ypotherical procein.
Fremyella diplosiphon (Calothrix PCC 7601).
Bacteria, Cyanobacteria, Nostocales; Microchaetaceae; Fremyella.
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Stowe-Evans E.L., Ford J., Kehoe D.M.;
"Genomic DNA Microarray Analysis: Identification of New Genes
Regulated by Light Color in the Cyanobacterium Fremyella
diplosiphon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.4%; Score 43.5; DB 2; Length 1993; 54.5%; Pred. No. 8.9e+02;
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                                                                                                               PRT; 1993 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
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                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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942 CGEWIESMWGC 952
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Best Local Similarity
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06H022
AC 06H020
AC 06H00
DT 05-JI
DT 0
                                               RESULT :
P90670
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EMBL, AE017203, AAS08923.1; -. InterPro; IPR004254; HHyIII. related.
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                                                                                                                                                Length 168;
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Stowe-Evans E., Ford J., Kehoe D.M.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, 74548455; AAT1947.1;
Hypochetical protein.
SEQUENCE 168 AA; 18932 MW; 1C9DB963D5210332 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Firmicutes, Lactobacillales, Lactobacillaceae, Lactobacillus.
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 AA; 24721 MW; IDBC78FF9810E152 CRC64;
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Last sequence update)
Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                             59.7%; Score 43; DB 2; I 66.7%; Pred. No. 1.1e+02; ative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.7%; Score 43; DB 2; I 62.5%; Pred. No. 1.4e+02; iive 2; Mismatches 1;
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TIGRFAMS; TIGR01065; hlyIII; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hemolysin-like protein.
OrderedLocusNames=LJ1101;
                                                                                                                                                                                               6, Conservative
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Matches 5, Conservative
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                                                                                                                                                                                                                                                                                           122 CGYWLSLRG 130
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172 GFWLLVWG 179
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                                                                                                                                                                 Best Local Similarity
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646 AA.

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PRELIMINARY;
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SEQUENCE 646 AA;
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Matches 5; Conserv
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                  Tl10923 protein
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QBDKD6
QBDKD6;
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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Dujon B., Sherman D., Fischer G., Neuveglise C., Talla B.,
Goffard N., Frangeul L., Aigle M., Anthousard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Janniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard E., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Pukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
M., Genome evolution in yeasts.;
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                                                                Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C., Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann B., Barrangou R., Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.; Inthe genome sequence of the probictic intestinal bacterium clactobacillus johnsonii NCC 533."; Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).

EMBL; AE017203; AAS08923.1. -. SEQUENCE 221 AA; 24721 MW; 1DBC78FF9810E152 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2004 (TrEMBLrel. 28, Created)
01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Chromosome B of strain CilB99 of Yarrowia lipolytica.
ORFNames-YALIDB20471g;
Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales; Dipodascaceae; Yarrowia.
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                                                                                                                                                                                                                                                                                   59.7%; Score 43; DB 2; Length 221; 62.5%; Pred. No. 1.4e+02; ive 2; Mismatches 1; Indels
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 501 AA; 56411 MW; 91F08EF5A63C60FB CRC64;
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Best Local Similarity 62.5
Matches 5; Conservative
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GYYLTLWYC 165
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                                                                                                                                                                                                                                                                                                                                                                                                                              172 GFWLLVWG 179
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Best Local Similarity
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  SEQUENCE FROM N.A.
                        STRAIN=NCC 533;
PubMed=14966310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CLIB99;
GENOLEVURES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CLIB99;
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A Nakamura Y., Kanko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
A Nakamura Y., Kanko T., Sato S., Ikeuchi M., Kishida Y.,
A Kitonabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
Kiyokawa C., Kohara M., Matsumoto M., Natsumo A., Nakazaki N.,
A Kingos S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
Thermosynechococcus alongatus BP-1.";
Thermosynechococcus alongatus BP-1.";
Thermosynechococcus alongatus BP-1.";
BMBL, AP005372; BAC08475.1;
CGO:0003824; F:catalytic activity; IEA.
RGO; GO:0003824; F:catalytic activity; IEA.
RGO; GO:0003824; PP2C-1ike.
R Fem; PF00481; PP2C; 1.
R SMART; SM00331; PP2C; 1.
R SMART; SM00331; PP2C_SIG; 1.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hyporhetical protein OJ1138_B05.118.
Name=OJ1138_B05.118;
Orza sativa (japonica cultivar-group).
Eukaryora, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 59.7%; Score 43; DB 2; Length 733; Best Local Similarity 85.7%; Pred. No. 4.2e+02; Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                                     OrderedLocusNames=tl10923;
Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasaki T., Matsumoto T., Katayose Y.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005486; BAC16197.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      646 AA; 71071 MW; 56C5A74F76652D56 CRC64;
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Pfam, PP04578; DUP594; 1.
Hypothetical protein.
SEQUENCE 733 AA; 82939 MW; E95884DAD1DC2AC9 CRC64;
                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             733 AA.
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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RESULT 10 Q8DKD6

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NCBI_TaxID=9606;
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The Perior Natl. Acad. Sci. U.S.A. 101:2530-2535 (2004).

The SIMILARITY: Contains 1 histidine kinase domain.

BEMBL. AX273869; AARP4165.1.

BEMBL. AX273869; AARP4165.1.

BO; GO:00016020; C:membrane; IEA.

GO; GO:0001537; F:NAT binding; IEA.

GO; GO:000156; F:Kinase activity; IEA.

GO; GO:000156; F:Kwo-component sensor molecule activity; IEA.

GO; GO:000156; F:two-component signal transduction system (p. ..; IEA.)

INTERPRO; IPR003594; ATPbind ATPase.

INTERPRO; IPR001501; His kinase.

INTERPRO; IPR001891; Response_reg.

INTERPRO; IPR00189; Response_reg.

INTERPRO; IPR001789; Response_reg.

INTERPRO; IPR001789; Response_reg.
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                                                                                                                                                                                                                         He J., Baldini R.L., Deziel E., Saucier M., Zhang Q., Liberati N.T., Lee D., Urbach J., Goodman H.M., Rahme L.G.; "The broad host range pathoden Feeudomonae aeruginosa strain PA14 carries two pathogenicity islands harboring plant and animal virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q96AC0;
Q1-DBC-2001 (TrEMBLrel. 19, Created)
01-DBC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
AGTRAP protein.
Homo sapiens (Human)
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 59.7%; Score 43; DB 2; Length 1084; Best Local Similarity 66.7%; Pred. No. 6e+02; Matches 6; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kinase; Phosphorylation; Sensory transduction; Transferase.
SEQUENCE 1084 AA; 119129 MW; C953FDD2F273BF1B CRC64;
                                                01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                           PRT; 1084 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probom; P000003; Response_reg; 1.
SMART; SM00387; HATPase c; 1.
SMART; SM00388; Hiska; 1.
SMART; SM00091; PAS; 1.
SMART; SM00091; PAS; 1.
PROSITE; PS50109; HIS KIN; 1.
PROSITE; PS50804; HPT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01627; Hpt; 1.
Pfam; PF00072; Response_reg; 1.
                                                                                                       Name=rcsC; ORFNames=RL038;
                           PRELIMINARY;
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                                                                                                                   Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 750 GAWLKAWGC 758
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                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                              STRAIN=PA14;
PubMed=14983043;
                                       Q7WY20;
                           Q7WY20
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RESULT 12
Q7WY20
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Q96AC0
AC Q96AC
AC Q96AC
DT 01-DB
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DT 01-DB
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MEDLINE=22389257; PubMed=12477932;

MEDLINE=22389257; PubMed=12477932;

MEDLINE=22389257; PubMed=12477932;

MISTAGRAN R.L., Fearbaold E.A., Grouse L.H., Derge J.G.,

Altachar R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altachar R.D., Marushia R., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marushia R., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Wullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glubs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.;

RA Gones S.J., Marra M.A.;

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Gones S.J., Marra M.A.;

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield W.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield W.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. R.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. R.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. R.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. R.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. R.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. R.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. R.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. R.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. R.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., B
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Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O., Rajkumar N., Yi Q., Nickerson D.A.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY488088; AAR25556.1; -.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IRR099436; AGTRAP.
Pfam; PF06396; AGTRAP; 1.

Receptor.
SEQUENCE 159 AA; 17419 MW; 7E1D5C7E79AE6BC5 CRC64;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.0%; Score 42.5; DB 2; Length 159; ilarity 70.0%; Pred. No. 1.2e+02; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.; Strausberg R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC017328; AAH17328.1; InterPro; IPR009436; AGTRAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 AA; 16669 MW; 637C01214175C3C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Angiotensin II receptor-associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF06396; AGTRAP;
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Best Local Similarity
7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9NRW9 PRELIMINARY; PRT; 159 AA.
Q9NRW9;
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ATRAP.
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14 GHWLLTTWGC 23
2 GYW-LTIWGC 10
|:| || || || 114 GHWLLTTWGC 23
                                                                                                                                                                                                                           RESULT 15
099NRW
AC 099NRW
AC 090NRW
DT 01-0C
DT 01-MA
DE ATRAP
OS HOMO
OC BUKAR
OC MARIMA
OC MARIMA
OC MARIMA
OC MARIMA
OC RESULA
RN (1)
RN (1)
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RN (1)
RN GENEW
DR GENEW
ON GENEW
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Search completed: December 30, 2004, 13:16:10 Job time : 94.2641 secs

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WPI; 2000-136888/12
                                                                                                                                                                                                                 RESULT 1
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VEGFR-3 b
Rhesue D
VEGFR-3 b
VEGFR-3 b
VEGFR-3 b
Haemophil
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Backbone
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Peptide #
Peptide #
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Human bra
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                                                            (without alignments)
31.578 Million cell updates/sec
                                                   3, 2005, 16:11:20 ; Search time 79.52 Seconds
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Abp53965 1
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Aam61892
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                  - protein search, using sw model
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AAB99769
AAO26093
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ABB19829
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ABB41036
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geneseqp2003as:*
geneseqp2003bs:*
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seq length: 200000000
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Match Length
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# ALIGNMENTS

Somatostatin analogue, therapy; cyclic peptide; autoimmune disease; endocrine disorder; cancer; diabetic-associated complication; diagnosis; gastrointestinal disorder; inflammatory disease; pancreatitis; atherosclerosis; restenosis; post-aurgical pain; VIP secretion inhibitor; hormone-secreting tumour; hormone-dependent tumour; diarrhoea; vasoactive intestinal peptide; non-insulin dependent diabetes mellitus. /note= "D-form residue" Location/Qualifiers Somatostatin analogue peptide 3181. Ş /note= "Trp-NH2" AAY76794 standard; peptide; 7 entry) (first Misc-difference Modified-site 20-APR-2000 Synthetic AAY76794;

WO9965508-A1 23-DEC-1999

99WO-IL000329 98US-00100360. 15-JUN-1999; 19-JUN-1998; 02-DEC-1998;

(PEPT-) PEPTOR

Gellerman G; Hornik V, Afargan MM, Cyclized somatostatin analogs for inhibiting growth hormone secretion from anterior pituitary and as antiproliferative agents for the treatment

Example 11; Page 61; 82pp; English.

This sequence represents a somatostatin analogue of the invention. The invention relates to a backbone cyclised somatostatin analogue that has

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one connected to a bridging group comprising an amide, thioseter connected to a bridging group comperient an amide, thiosether, thioseter or disulphide. At least one building unit is connected via a bridging corporate control or a cyclic structure with a moiety selected from a second building unit, side chain of or N-terminal amino acid residue. A composition containing the analogue may be used for preventing disorders such as cancers, autofimmune diseases, endocrine disorders, diabeticas unit may also be used for disagnosing cancer. The backbone cyclic pain. It may also be used for disagnosing cancer. The backbone cyclic analogue is used for imaging the existence of metastases. Somatostatin analogues can be used for the treatment patients with hormone-secreting and parameter tumours. They reduce diarrhoea through the inhibition of vascactive intestinal peptide (VIP) secretion and by direct effect on intestinal secretion. Somatostatin analogues selective to type 2 and 5 receptors may be used for treatment of non-insulin dependent diabetes mellitus. They are useful for the prevention of atherosclerosis and restenosis. The analogues are metabolically stable, selective in their in-vivo activities and safe
      building unit containing a nitrogen atom of the peptide backbone
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Sequence 7 AA;

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; Score 38; DB 3; Length 7; Pred. No. 1.7e+06; 3; Mismatches 0; Indels
 100.0%;
57.1%; F
 Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                 GYWXXXW 7
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GYWKVCW 7
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Gaps

ABP53964 standard; peptide; 7 AA. 09-JAN-2003 (first entry) ABP53964; RESULT 2 ABP53964 THE STATE OF STATE OF STATE OF STATES OF STATE

VEGFR-3 binding peptide SEQ ID NO:67.

Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; anglogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antiidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.

Homo sapiens. Synthetic.

/note= "X is any amino acid" Location/Qualifiers Misc-difference 4.

WO200257299-A2

25-JUL-2002.

17-JAN-2001; 2001US-0262476P.

16-JAN-2002; 2002WO-IB000099.

(LUDW-) LUDWIG INST CANCER RES (LICN ) LICENTIA LTD.

Kubo H; Alitalo K, Koivunen E,

WPI; 2002-691521/74.

New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.

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The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have eyeostatic, heatoropic, antiinflammatory, hypotenasive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicit, ovary, skin, head and neck, osecophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic; somatotropin release inhibiting factor; somatostatin receptor subtype; synthesis; antiarteriosclerotic; immunosuppressive; cytostatic; cancer; antidiabetic; antiinflammatory; somatostatin receptor ligand; atherosclerosis; autoimmune disease; diabetic-associated complication; endocrine disorder; inflammation; gastrointestinal disorder; restenosis;
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                 Length 7;
                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Backbone cyclised somatostatin analogue PTR 3181.
                                                                                                                                                                                                                                                                                                                                 100.0%; Score 38; DB 5; I
100.0%; Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fluorenylmethoxycarbonyl)"
                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
             Claim 21; Page 81; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP53418 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pancreatitis; post-surgical pain
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99WO-IL000329.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
les 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HORN/) HORNIK V.
(AFAR/) AFARGAN M M.
(GELL/) GELLERMAN G.
                                                                                                                                                                                                                                                                                                                                                                                                   1 GYWXXXW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                  GYWXXXW 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2002052315-A1
                                                                                                                                                                                                                                                                                                 Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .9-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP53418;
                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                   Matches
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(LUDW-) LUDWIG INST CANCER RES (LICN ) LICENTIA LTD.
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   WPI; 2002-681319/73
                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                    Misc-difference 4.
                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                      WO200257299-A2
                                                                                               Sequence 7 AA;
                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                              25-JUL-2002
                                                                                                                                                                                                         Synthetic
                                                                                                                                                      ABP53965;
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The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have eytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and wulnerary activities, and can be used in gene therapy. diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oseophagus, bone, marrow or blood, and diseases of enronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; anglogenesis; lymphanglogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; pDGF; platelet derived growth factor.
                                                                                                                    New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 38; DB 5; I
100.0%; Pred. No. 1.7e+06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEGFR-3 binding peptide SEQ ID NO:36.
                                                                                                                                                                                                                   Claim 22; Page 81; 149pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP53933 standard; peptide; 9 AA.
                       Kubo H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LUDW-) LUDWIG INST CANCER RES (LICN ) LICENTIA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JAN-2002; 2002WO-IB000099.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
                       Alitalo K, Koivunen E,
                                                                   WPI; 2002-691521/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                  The present invention describes backbone cyclised somatostatin analogues

(I) that incorporates at least one building unit containing one nitrogen
atom of the peptide backbone connected to a bridging group (comprising an
amide, thioether, thioester or disulfide) where at least one building
unit is connected via the bridging group to form a cyclic structure with
a moiety selected from the group consisting of a second building unit,
the side chain of an amino acid residue of the sequence or the N-terminal
amino acid residue. (I) has antiatteriosclerotic, immunosuppressive,
cytostatic, antidiabetic, antiinflammatory and analgesic activities, and
can be used as a somatostatin receptor ligand. (I) are useful in the
treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-
associated complications, endocrine diseases, ancers, diabetic-
gastrointeetinal disorders, pancreatitis, post-surgical pain, and
gastrointeetinal also be used in the disgnosis of cancer, by imaging
the existence of metastases, it being labeled with a detectable probe.
The present sequence represents a backbone cyclised somatostatin analogue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; anglogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                   useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                               and cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 38; DB 5; Length 7; Pred. No. 1.7e+06; 3; Mismatches 0; Indels
                                                                New backbone cyclized somatostatin analogs are e.g. treatment of atherosclerosis, autoimmune diseases an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "X is any amino acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                           Example 12; Page 21; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP53965 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
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New isolated peptide that inhibits VEGF-C and VEGF-D, useful for

Kubo H;

Alitalo K, Koivunen E,

WPI; 2002-691521/74

ö

Gaps

ö

Length 8; 0; Indels

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                                                                           The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotenaive, antidiabetic and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, piver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemanglomas and diabetes. The present sequence
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diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhesus D antibody binding peptide; Rhesus D; RhD; identification; anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy; prophylaxis; haemolytic disease of the newborn; HDN; ITP; idiopathic thrombocytopaenic purpura; immunoglobulin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB99759 standard; peptide; 10 AA.
                                                 Claim 14; Page 80; 149pp; English
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Best Local Similarity
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2 GYWWDTW
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The present sequence represents a peptide capable of binding Rhesus D antibodies (I). Also described in the present invention are: (I) a nucleic acid (II) encoding (I), (2) a vector (III) comprising one or more (II) operably linked to an expression control system; (3) a cell (IV)

Claim 1; Page 12; 19pp; English.

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peptides having immunologic properties of Rheaus D protein epitopes comprising any antibody/antibody fragment recognising an epitope of Rheaus D protein to several panning rounds with a phage display library, and identifying immunogenic peptide sequences which are mimotopes which differ in their amino acid sequence from the amino acid sequences of Rheaus D protein; and (6) peptides (V) with immunological properties of Rheaus D protein epitopes obtained by (M1). (I) is used to manufacture an agent for the diagnosis, therapy or prophylaxis of manufacture an agent for the diagnosis, therapy or prophylaxis of newborn (HDN) or idiopathic thrombocytopaenic purpura (ITP), for the manufacture of an affinity reagent for anti-Rheaus D antibodies purified or removed from body fluids or immunoglobulin preparations. Using (I) as an immunogen to raise anti-Rheaus D antibodies avoids using immunisation with foreign erythrocytes thereby avoiding the risk of transmission of viral diseases like AIDS and hepatitis B
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comprising (II) or (III); (4) preparing (I); (5) identifying
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3; Mismatches
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Best Local Similarity
Matches 4; Conserv
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1 GYWSAKW
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                                                          The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotenaive, antiinflammatory, hypotenaive, antiinflammatory, hypotenaive, antiinflammatory, hypotenaive, compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, sakin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases. The present sequence chronic hepatitis, haemangiomas and diabetes. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; anglogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic, antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
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Claim 12; Page 80; 149pp; English,
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Best Local Similarity
Matches 4; Conserv
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The present invention describes an isolated peptide (1) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (1) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, puncr spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a VEGFR-3 binding peptide, which is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; anglogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
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Disclosure; Page 147; 149pp; English.
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Best Local Similarity 100.
Matches 7; Conservative
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be determined directly. The method can also be used to identify new inhibitory ligands of specific target proteins. The method provides high throughput screens which are essentially identical for similar and dissimilar targets, bypassing the need to develop distinct assays for biochemically diverse targets

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Gaps

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0; Indels

Length 11;

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; Score 38; DB Pred. No. 48; 3; Mismatches

100.0%; 57.1%;

Query Match Best Local Similarity

Sequence 11 AA;

8886666

4; Conservative

Matches

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|||:::| GYWWPDW 7 1 GYWXXXW 7

ADJ25827 standard; peptide; 11 AA.

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biological activity of a target protein (T) by inhibiting the binding of (T) biological activity of a target protein (T) by inhibiting the binding of (T) to a binding partner. The method comprises: (a) screening a first combinatorial library comprising first member ligands for binding to the target-binding ligands (TBLs), to identifying one or more TBLs; (b) screening a second library comprising second member ligands for the billity to inhibit the binding of one or more of the TBLs to the target protein, and so obtaining one or more inhibitory ligands; and (c) determining which of the inhibitory ligands can mediate a biological activity of the target protein. The present sequence represents a potential binding peptide for Haemophilus influenzae tyrosine tRNA synthetase from an example of the present invention. The method can be target protein. It can be used to identify the biological activity of a target protein whose biological function is not known and perhaps cannot
                                                                                                                                                                                                                                                                                    ;
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                   of
             diagnosing, evaluating and treating disorders mediated by the activity the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovar, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying ligands which mediate biological activity of a protein - by identifying target-binding ligands and screening a library for ligands which inhibit target-binding ligand mediated activity.
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae tyrosine tRNA synthetase binding peptide 21.
 invention are useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identification; ligand; biological activity; target-binding; drug screening; library; inhibitory ligand.
                                                                                                                                                                                                                                            100.0%; Score 38; DB 5; Length 10;
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Frelinger JA, Hyde-Deruyscher RP;
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                                                                                                                                                                                                                                                              Pred. No. 44;
3; Mismatches
Compositions and methods from the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW62148 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US019638
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                                                                                                                                                                                                                                                                57.1%;
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                                                                                                                                                                                                                                                                                    4; Conservative
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Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fowlkes DM, Kay BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-272389/24
                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           GYWLTIW
                                                                                                                                                                                                                                                                                                                       GYWXXXW
                                                                                                                                                                                                           Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                              Identification of ligand that can mediate biological activity of target protein, comprises screening first combinatorial library having first member ligands for binding to target protein to identify target-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                     ligand identification; peptide library; cyrosine tRNA synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 8; Length 11;
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                                                                                                                                                                                                                                                                                                                                                                      Frelinger JA, Hyde-Deruyscher RP;
                                                                           Tyrosine tRNA synthetase binding peptide #21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         %; Score 38; DB; Pred. No. 48; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5; SEQ ID NO 87; 98pp; English.
                                                                                                                                                                                                                                                                          96US-00740671.
97WO-US019638.
98US-00050359.
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57.18; I
                                                                                                                                                                                                                                               98US-00069827.
                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                      Kay BK,
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-068186/07.
                                                                                                                                                                                                                                                                                                                                       (KARO-) KARO BIO AB.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention
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                                                                                                                                                                                   US6617114-B1
                                                                                                                                                                                                                                               30-APR-1998;
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                                           20-MAY-2004
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                                                                                                                                                     Synthetic.
            ADJ25827;
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Indels

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Pred. No. 53; 3; Mismatches Score 38;

Length 12;

В

100.08;

57.1%;

Query Match Best Local Similarity Matches 4; Conserv

4; Conservative

1 GYWXXXW 7

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The present invention describes peptides capable of binding Rhesus D antibodies (I). Also described in the present invention are: (1) a nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more (C (III) operably linked to an expression control system; (3) a cell (IV) comprising (II) or (III); (4) preparing (I); (5) identifying (M1) cc (omprising subjecting an antibody/antibody fragment recognising and cepttope of Rhesus D protein to several panning rounds with a phage coptopes which differ in their aminoacid sequence from the amino acid sequences of Rhesus D protein; and (6) peptides (V) with immunological properties of Rhesus D protein; and (6) peptides (V) with immunological properties of Rhesus D protein epitopes obtained by (M1). (1) is used to coppertie of an agent for the diagnosis, therapy or prophylars of the monogen to raise anti-Rhesus D antibodies purpura (ITP), for the companies of an affinity reagent for anti-Rhesus D antibodies purified or removed from body fluids or immunoglobulin preparations. Using (I) as an immunogen to raise anti-Rhesus D antibodies avoids using immunisation with Rhesus D (RhD) antibody related peptide which is used in an anti-Rhesus D (RhD) antibody related peptide which is used in an anti-Rhesus D (RhD) antibody related peptide which is used in an anti-Rhesus D (RhD) antibody related peptide which is used in an anti-Rhesus D (RhD) antibody related peptide which is used in an anti-Rhesus D (RhD) antibody related peptide which is used in an anti-Rhesus D (RhD) antibody related peptide which is used in an anti-Rhesus D (RhD) antibodies avoids using in an anti-Rhesus D (RhD) antibodies perises or related peptide which is used in an anti-Rhesus D (RhD) antibodies perises or related peptide which is used in an anti-Rhesus D (RhD) antibodies perises and related peptide which is used in an anti-Rhesus D (RhD) antibodies perises and related peptide perises 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel peptides capable of binding Rhesus D antibodies are used to manufacture an agent for the diagnosis, therapy or prophylaxis of diseases associated with Rhesus D antigen, e.g. hemolytic disease of newborn (HDN).
                                                                                                                                                                                                                                                                                                                                                         Rhesus D antibody binding peptide; Rhesus D; RhD; identification; anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy; prophylaxis; haemolytic disease of the newborn; HDN; ITP; cyclic; idiopathic thrombocytopaenic purpura; immunoglobulin; dircular.
                                                                                                                                                                                                                                                                                                              Rhesus D antibody related peptide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .12
                                                                                                                                                                AAB99769 standard; peptide; 12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miescher S, Hofmann A, Fisch I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 8; 19pp; English
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                                                                                                                                                                                                                                                               21-SEP-2001 (first entry)
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                           CYWWPDW .
GYWXXXW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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Sequence 12 AA;

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                                                                                                                                                                                                        Immunoglobulin Fc region; binding; whole blood; plasma; transgenic milk; antibody response; half-life; stability; circulatory system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptides, useful as binding molecules for detecting, isolating purifying immunoglobulin Fc-region polypeptides present in a solution, for regulating or preventing an antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Potter MD;
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38;
                                                                                                                                                                              73.
                                                                                                                                                                                                                                                                                                                                                                                                                    Stochl M,
                                                                                                                                                                              Fc region binding peptide SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADJ50760 standard; peptide; 13 AA.
                                                                                            AAO26093 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 76; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.08;
                                                                                                                                                                                                                                                                                                                                     18-APR-2002; 2002WO-US012492.
                                                                                                                                                                                                                                                                                                                                                               18-APR-2001; 2001US-0284534P.
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                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-201220/19.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          (DYAX-) DYAX CORP
                        GYWSAKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13 AA;
                                                                                                                                                                                                                                                                               WO200286070-A2
                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                    03-APR-2003
                                                                                                                                                                                                                                                                                                         31-OCT-2002
                                                                                                                        AA026093;
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Matches
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31-JAN-2002.

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The invention relates to a method of evaluating sample by providing a soluble serum protein (I), one or more compounds physically associated with (I), and a (I)-binding agent that comprises,a peptide that specifically binds to (I), allowing the (I)-binding agent to bind to to form a complex including one or more compounds physically associated with (I), separating the complex from one or more compounds of the sample, and evaluating one or more of the physically associated compounds. The sample comprises blood or serum, or is obtained from a biopsy. The sample may also be obtained from a tumour or a region within modulate interaction of serum protein-binding compound and serum protein and for identifying binding ligands for serum protein. The present
                                                                                                                                                                                                                                                                                                                                           Evaluating sample comprising soluble serum protein by forming complex comprising serum protein and physically associated compounds using peptide ligand that specifically binds with proteins, which is separated
                                                human serum albumin; HSA; serum; blood; tumour; human.
               Human serum albumin binding peptide, Seq ID No 297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Scor.
57.1%; Pred. No. 5',
                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 297; 191pp; English.
                                                                                                                                                                                16-JUN-2003; 2003WO-US018896
                                                                                                                                                                                                                L4-JUN-2002; 2002US-0388642P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 57.1
nes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        method of the invention.
                                                                                                                                                                                                                                                                                Dawson BM;
                                                                                                                                                                                                                                                                                                             WPI; 2004-082161/08.
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                                                                                                               WO2003106493-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                            and evaluated
                                                                                  Homo sapiens
                                                                                                                                                24-DEC-2003
                                                                                                                                                                                                                                                                                Sato AK,
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Score 38; DB 8; Length 13; Pred. No. 57; 0; Indels

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Gaps

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AAU93268 standard; peptide; 16 AA. 02-JUL-2002 (first entry) AAU93268; RESULT 15 AAU93268 

Granulocyte-colony stimulating factor receptor binding peptide #74. G-CSFR; granulocyte-colony stimulating factor receptor; cytokine; haematopoietic growth factor; neutrophil proliferation; AIDS; neutrophil differentiation; acquired immunodeficiency syndrome; chemotherapy-induced neutropaenia; community acquired pneumonia; depressed neutrophil count; immunostimulant.

Synthetic

WO200207676-A2

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bind specifically to G-CSFR and allow for studies of biological activities mediated by the receptor and for the treatment of diseases, disorders and conditions that would benefit from activating or inactivating G-CSFR. The present sequence is a G-CSFR binding peptide of
                                                                                           Novel compounds, useful for treating depressed neutrophil count, comprist peptide chains of approximately 6 to 40 amino acids in length that bind to granulocyte-colony stimulating factor receptor.
                                                           Cwirla SE, Balu P, Duffin DJ, Piplani S, Mceowen-Merrill B;
Schatz PJ;
                                                                                                                      Claim 4; Page 53; 90pp; English.
                  20-JUL-2001; 2001WO-US023046.
                                20-JUL-2000; 2000US-00620091.
                                             (GLAX ) GLAXO GROUP
                                                                               WPI; 2002-329382/36.
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Sequence 16 AA;

Gaps ; 0 100.0%; Score 38; DB 5; Length 16; 57.1%; Pred. No. 70; ive 3; Mismatches 0; Indels 4; Conservative Best Local Similarity
Matches 4; Conser

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Search completed: January 3, 2005, 16:27:22 Job time: 81.52 secs

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TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 87:
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202) 737-3
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
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Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 26841, A
Sequence 26841, A
Sequence 6, Appl
Sequence 6, Appl
Sequence 6868, Ap
Sequence 23128, A
Sequence 23128, A
Sequence 21318, A
Sequence 1518, A
Sequence 1867, A
Sequence 1867, A
Sequence 1867, A
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4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 87, Appl
Sequence 81, Appl
Sequence 7620, Ap
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23.027 Million cell updates/sec
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                                                                                               January 3, 2005, 16:19:47; Search time 20.16 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/1/iaa/SA_COMB.pep:*
/cgn2_6/ptodata/1/iaa/SB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/GA_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RB_CTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-145-828A-11
US-09-903-456-11
US-09-252-991A-26841
US-09-252-991A-3031
US-09-252-991A-3031
US-09-107-532A-6868
US-09-107-532A-6868
US-09-107-532A-6945
US-09-252-991A-213128
US-09-252-991A-19339
US-09-252-991A-19339
US-09-252-991A-18697
US-09-252-991A-19339
US-09-252-991A-1839
US-09-252-991A-18697
US-09-252-991A-1839
US-09-270-767-6015
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US-09-620-091-81
US-09-543-681A-7620
US-09-502-653-10
US-09-610-906-12
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US-09-621-976-7633
US-09-374-135-4
US-09-270-767-35277
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                                                                                                                                                                                                                                                                                    478139 seqs, 66318000 residues
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                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                - protein search, using sw model
                                                                                                                                                                                                                                ABLOSUM62DX Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                US-10-046-922-67
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Match Length
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                                                                  OM protein
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2, Appli
8752, Ap
20388, A
45223, A
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18939, A
6324, Ap
479, App
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16589, A
28537, A
61294, A
45772, A
                                                     Sequence
Seq
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                            Sequence
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KAY, Brian K
FRELINGER, Jeffrey A
HYDE-DENTYSCHER, Robin P
TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING
COMPLEMENTARY COMBINATORIAL LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CUNTRY: U.S.A.

ZIP: 20001

COUNTRY: U.S.A.

ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/069,827A

PILING DATE: 30-Apr-1998

CLASSIFICATION NUMBER: US/09/069,827A

PRIOR APPLICATION NUMBER: US/09/069,359

FILING DATE: 31-ARR-1998

APPLICATION NUMBER: PCT/US9/1/9638

PILING DATE: 31-OCT-1997

APPLICATION NUMBER: US 08/740,671

PILING DATE: 31-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVET P

REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: 28,005

TELERCHOMENICATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: POWLKES-4C

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEBRONE (202) 622-5197
                                                                                               US-09-270-767-4523

US-09-452-937A-34

US-09-48-198-198-19839

US-09-198-452A-479

US-09-198-452A-479

US-09-270-767-43086

US-09-270-767-43086

US-09-270-767-45283

US-09-270-767-61294

US-09-270-767-61294

US-09-770-767-61294

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US-09-770-770-770-86

US-09-770-770-86
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CORRESPONDENCE ADDRESS:
ADDRESSE: REWONY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street N.W., Suite 300
                                               -09-489-039A-8752
-09-248-796A-20388
-09-270-767-45223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 87, Application US/09069827A Patent No. 6617114 GENERAL INFORMATION:
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US-09-069-827A-87
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US-09-069-827A-87

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CTHER INFORMATION: GenBank ID No. 6566066: g2346968;
PUBLICATION INFORMATION:
US-09-610-906-12
                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bj rnvad, Mads Eskelund
APPLICANT: Glausen, ib Groth
APPLICANT: Schlein, Martin
APPLICANT: Schlein, Martin
APPLICANT: Bech, Lisbeth
APPLICANT: Bech, Lisbeth
APPLICANT: Stergaard, Peter Rabbek
APPLICANT: Stergaard, Peter Rabbek
APPLICANT: Sj holm, Carsten
APPLICANT: Sj holm, Carsten
CURRENT SPLICATION: NOVBER: 08/05/02,653
CURRENT APPLICATION NUMBER: PA 1999 00184
BARLIER FILLING DATE: 1999-06-07
EARLIER FILLING DATE: 1999-06-07
EARLIER FILLING DATE: 1999-03-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Walker, Michael G.
APPLICANT: Volkmuth, Wayne
APPLICANT: Klinger, Tod M.
FILE REFERENCE: PC-0012 CIP
CURRENT APPLICATION NUMBER: US/09/610,906
CURRENT FILING DATE: 2000-07-06
PRIOR PILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PERL PROGram
SEQ ID NO 12
LENGTH: 263
                                                                            US-09-502-653-10
; Sequence 10, Application US/09502653
; Patent No. 6331426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/09610906 Patent No. 6566066
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ORGANISM: Rattus norvegicus
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Best Local Similarity 57.1.
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210 GYWEPAW 216
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Patent No. 6605709
GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR OF FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                            Sequence 81, Application US/09620091

| Sequence 81, Application US/09620091
| Patent NO. 6716811
| GENERAL INFORMATION:
| APPLICANT: BALU, PALANI
| APPLICANT: BALU, DAVID J.
| APPLICANT: BILU, DAVID J.
| APPLICANT: PIPLANI, SUNILA
| APPLICANT: PIPLANI, SUSPENION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
| TITLE OF INVENTION: USES
| FILE REFERENCE: 0300-0014
| CURRENT FILING DATE: 2000-07-20
| NUMBER OF SEQ ID NOS: 491
| SOFTWARE: PatentIn Ver. 2.1
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100.0%; Score 38; DB 4; Length 11; 57.1%; Pred. No. 22; ive 3; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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US-09-543-681A-7620
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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  Query Match
Best Local Similarity
Matches 4; Conser
                                                                                                                GYWXXXW 7
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GYWWPDW 7
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GYWCDPW 7
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US-09-252-991A-26841

US-09-252-991A-26841

Sequence 26841, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

PAPPLICANTON:

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26841

LENGTH: 339
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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57.1%; Pred. No. 5.38+02;
ive 3; Mismatches 0; Indels
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                              APPLICANT: ADDOLT LAUGULALOLANDER
APPLICANT: Mukerji, Pradip
APPLICANT: Huang, Yung-Sheng
APPLICANT: Huang, Yung-Sheng
APPLICANT: Huang, Yung-Sheng
TITLE OF INVENTON: BLONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT FILING DATE: 2001.07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-00-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 278
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4.4e+02;
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Pred. No. 4.4e
3; Mismatches
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ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%;
Best Local Similarity 57.1%;
Matches 4; Conservative 3;
                         APPLICANT: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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108 GYWIFLW 114
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                                                                                                                                        Sequence 15791, Application US/09248796A

Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT PILING DATE: 1999-02-12
PRIOR PELIOR DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 15791
LENGTH: 274
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4.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mikerji, Pradip
APPLICANT: Huang, Ving-Shang
APPLICANT: Huang, Ving-Shang
APPLICANT: Huang, Ving-Shang
APPLICANT: Thurmond, Jennifer
APPLICANT: Thurmond, Jennifer
APPLICANT: Kirchner, Stephen J.
APPLICANT: Kirchner, Stephen J.
TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
TILE REFERENCE: 6407.US.01
CURRENT APPLICATION NUMBER: US/09/145,828A
CURRENT APPLICATION NUMBER: 1998-09-02
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 4.46
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/09145828A
Patent No. 6403349
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
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US-09-903-456-18
; Sequence 18, Application US/09903456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
57.1%; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
                         224 GYWDFHW 230
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108 GYWIFLW 114
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84 GYWPITW 90
1 GYWXXXW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                         RESULT 6
US-09-248-796A-15791
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US-09-145-828A-11
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MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Cry
FEATURE:
                                                                                           , NAME/KEY:
, NAME/KEY:
US-08-415-751-6
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Patent No. 5643772

GENERAL INFORMATION:
APPLICANT: BETERSEN, CAROLYN
APPLICANT: BEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: WELSON, CRETCOR AND TITLE OF INVENTION: WETHODS FOR IMMUNOTHERAPY AND TITLE OF INVENTION: METHODS FOR IMMUNOTHERAPY AND TITLE OF INVENTION: DAGNOSIS AND KIT
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
STATE: California
COUNTRY: United States of America
ZIP: 94306-1840
COMPUTER FRADABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: PHILLIPS, MOORE, LEMPIO & FINLEY 385 Sherman Avenue, Suite 6
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION WUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; RICH APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                480.19-2 (HHD)
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SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,751
FILING DATE: 03-APR-1995
CLASSIFICATION 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/071,880
FILING DATE: June 1, 1993
APPLICATION NUMBER: 07/891,301
FILING DATE: May 29, 1992
ATTORNEY/ACENT INFORMATION:
NAME: Hana Dolezalova
                                                                                                                                                                                                                                                           ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32031
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INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (415) 324-1677
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linear
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315 GYWRGPW 321
                                                                                                                                                                                                                                                                                                                                                                                                                          1 GYWXXXW 7
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Sequence 15188, Application US/09248796A

Sequence 15188, Application US/09248796A

Sequence 15188, Application US/09248796A

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT PILING DATE: 1999-02-12

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 15188

LENGTH: 367
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US-09-107-532A-6868
US-09-107-532A-6868

Sequence 6868, Application US/09107532A

Sequence 6868, Application US/09107532A

Sequence 6868, Application US/09107532A

Sequence 6868, Application US/09107532A

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
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                                                                                                           Positions coded by nonsense codons are identified as Xaa.
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                         100.0%; Score 38; DB 1;
57.1%; Pred. No. 5.7e+02;
iive 3; Mismatches 0;
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57.1%; Pred. No. 5.7e+02;
iive 3; Mismatches 0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
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MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
COMPANING SYSTEM: <Unknown>
                                                               Cryptosporidium parvum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 57.1
Matches 4; Conservative
..rs: peptide
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216 GYWWLTW 222
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276 GYWLVDW 282
                                                                                                                                                                                                                                                                                                            1 GYWXXXW 7
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LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                  |||:::|
112 GYWLTCW 118
                                                                                                                 ORIGINAL SOURCE:
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111 GYWISAW 117
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                                                                                                                                                           FEATURE
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Patent No. 6583275

GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEBHONE: (781)893-5007
TELEPAX: (781)893-507
INFORMATION FOR SEQ ID NO: 6868:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ) NAME/KEY: misc feature
) LOCATION: (B) LÖCATION 1...478
; SEQUENCE DESCRIPTION: SEQ ID NO: 6868:
US-09-107-532A-6868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: «Unknown»
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TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                 LENGTH: 478 amino acida
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 6945: SEQUENCE CHARACTERISTICS:
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 7310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||:::|
98 GYWLSAW 104
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US-09-107-532A-6945
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Sequence 23328, Application US/09252991A
; Sequence 23328, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
    APPLICANT: Marc J. Rubenfield et al.
    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR PILING DATE: 1998-02-18
; PRIOR PILING DATE: 1998-02-18
; PRIOR PILING DATE: 1998-02-17
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23328
LENGTH: 499
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                                                                                                                                                                                            Query Match 100.0%; Score 38; DB 4; Length 492; Best Local Similarity 57.1%; Pred. No. 7.5e+02; Matches 4; Conservative 3; Mismatches 0; Indels
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                              ;
NAME/KEY: misc_feature
;
LOCATION: (B) LOCATION 1...492
;
SEQUENCE DESCRIPTION: SEQ ID NO: 6945:
US-09-107-532A-6945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: January 3, 2005, 16:33:49 Job time : 21.16 secs
ORGANISM: Enterococcus faecium
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Sequence 324628, Sequence 362818, Sequence 176036,

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Sequence

Sequence

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Sequence 17, Appl Sequence 21, Appl Sequence 25, Appl Sequence 33, Appl Sequence 37, Appl Sequence 41, Appl Sequence 41, Appl Sequence 6, Appl Sequence 17356, Sequence 260243, Sequence 260243, Sequence 86, Appl Sequence 86, Appl

12, Appl 267810, 64263,

Sequence

Sequence

Sequence 5 Sequence 5 Sequence 6 Sequence 1

е 6

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Sequence 67, Application US/10046922;
Publication No. US20020164667A1;
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGETA:
TITLE OF INVENTION: VEGETA:
FILE REFERENCE: 2896/37084A
CURRENT FLING DATE: 2002-01-15;
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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; LOCATION: (4)...(6)

; OTHER INFORMATION: X at position 4-6 is any amino acid

US-10-046-922-67
               US-10-425-115-324628

US-10-425-115-324628

US-10-424-599-240891

US-10-424-599-252989

US-10-424-599-252989

US-10-424-599-252989

US-10-36-493-19264

US-09-910-483-15

US-09-910-483-13

US-09-910-483-13

US-09-910-483-13

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US-09-910-483-21

US-09-910-483-21

US-09-910-483-33

US-09-910-483-41

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US-09-910-483-41

US-09-910-483-41

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US-09-910-483-41

US-10-425-115-260243

US-10-425-115-357518

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US-10-425-115-357518

US-10-425-115-35718

US-10-425-115-35718
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100.0%; Pred. No. 1.5e+06;
ive 0; Mismatches 0;
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; Sequence 68, Application US/10046922
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Best Local Similarity 100.
Matches 7; Conservative
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GYWXXXW
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ORGANISM: peptide
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Sequence 36, Appl
Sequence 35, Appl
Sequence 73, Appl
Sequence 73, Appl
Sequence 297, Appl
Sequence 297, Appl
Sequence 2127, Appl
Sequence 2127, Appl
Sequence 2127, Appl
Sequence 2127, Appl
Sequence 21762, Sequence 21762, Sequence 21762,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                 January 3, 2005, 16:32:45; Search time 70.56 Seconds (without alignments) 35.687 Million cell updates/sec
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(ggn2_6/ptodata/2/pubpaa/US06_PUBCOMB. DEPT.*

(ggn2_6/ptodata/2/pubpaa/US06_PUBCOMB. DEPT.*

(ggn2_6/ptodata/2/pubpaa/US07_NEW_PUB. DEPT.*

(ggn2_6/ptodata/2/pubpaa/US07_NEW_PUB. DEPT.*

(ggn2_6/ptodata/2/pubpaa/US08_PUBCOMB. DEPT.*

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(ggn2_6/ptodata/2/pubpaa/USS0_NE
                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 US-10-046-922-68
3 US-10-046-922-36
3 US-10-046-922-36
3 US-10-046-922-34
3 US-10-046-922-34
4 US-10-125-869A-73
4 US-10-125-869A-73
4 US-10-125-869A-73
5 US-10-462-262-27
7 US-10-864-761-35127
US-09-864-761-35127
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US-09-864-761-35127
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                                                                                                                                                                                                                                                                                                                                                                                                1599051 seqs, 359727711 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                              Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
                                                                                                                                                                                                                                                                                     1 GYWXXXW 7
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                                                                                                                                                                                                                                                                                          Sequence:
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Gaps

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Length 7; Indels

Result

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100.0%; Score 38; DB 13;
57.1%; Pred. No. 1.2e+02;
iive 3; Mismatches 0;
                                                                                                                  ORGANIEM: isolated peptide
FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(1)
OTHER INFORMATION: X is any amino acid
LOCATION: (10)..(10)
COTHER INFORMATION: X is any amino acid
GOTHER INFORMATION: X is any amino acid
US-10-046-922-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 73, Application US/10046922 Publication No. US20020164667A1
    2002-01-15
80
CURRENT FILING DATE: 2002-01-1
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 34
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: isolated peptide
                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
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Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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2 GYWLTIW 8
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GYWLTIW 8
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                                                                                                     TYPE: PRT
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Sequence 36, Application US/10046922

Publication No. US20020164667A1

GENERAL INFORMATION:

APPLICANT: Alitalo, Karii

APPLICANT: Kubo, Hajime

TITLE OF INVENTION: VEGER-3 INHIBITOR MATERIALS AND METHODS

FILE REPERBENCE: 28967/37084A

CURRENT FILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin version 3.0

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 38; DB 13; Length 8; 100.0%; Pred. No. 1.5e+06; Live 0; Mismatches 0; Indels
                             APPLICANT: Alitalo, Kari
APPLICANT: Alitalo, Kari
APPLICANT: Kolounen, Erkki
APPLICANT: Kolounen, Erkki
APPLICANT: Kolounen, Erkki
APPLICANT: Kolounen, Erkki
APPLICANT: Kolounen, Erki
APPLICANT: Kolounen, Erki
APPLICATION UNGRER-3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 28967/37084A
CURRENT FILING DATE: 2022-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 68
LENGTH. 8
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US-10-046-922-34
US-10-046-922-34
Sequence 34, Application US/10046922
Sublication No. US20020164667A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 2896/137084A
CURRENT APPLICATION NUMBER: US/10/046,922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 38; DB 13; Length 9; 57.1%; Pred. No. 1.5e+06;
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3; Mismatches
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OTHER INFORMATION: X is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (8)..(8)
OTHER INFORMATION: X is any amino acid
Publication No. US20020164667A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 7; Conservative
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Matches 4; Conserv
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2 GYWWDTW 8
                                                                                                                                                                                                                                                                               ORGANISM: peptide FEATURE:
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US-10-046-922-36
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Sequence 35, Application US/10046922

Publication No. US2020164667A1

Sequence 35, Application US/10046922

Publication No. US2020164667A1

APPLICANT: Alitalo, Kari

APPLICANT: Kubo, Halime

TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS

TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS

CURRENT APPLICATION WUMBER: US/10/046,922

CURRENT FILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin version 3.0

SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Alitalo, Kari
APPLICANT: Alitalo, Kari
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
FILE REPREBNCE: 28967/37084A
CURRENT PILICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 73
LENGTH: 10
Length 10;
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                                                    0; Indels
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Tue Jan

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. Sequence 35127, Application US/09864761
, Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
NAME/KEY: MISC_PEATURE
CTHER INFORMATION: Tiel-20C-3-D116
US-10-280-066-476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 537
SOFTWARE: Patentin version 3.1
SEQ ID NO 476
LENGTH: 25
                                                                                          Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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6 GYWGELW 12
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                    1 GYWXXXW 7
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; FEATURE:
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                                                                                                                                                                                      100.0%; Score 38; DB 13; Length 10; 100.0%; Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 73, Application US/10125869A
; Bublication No. US2030199671A1
; GENERAL INFORMATION:
    APPLICANT: ROOMON, Isaac Jesus
    APPLICANT: Ru, Qi-Long
    APPLICANT: Ru, Qi-Long
    APPLICANT: Ransohoff, Thomas C.
    TILE OF INVENTION: BINDING MOLECULES FOR FC-REGION
    TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
    TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
    TITLE OF INVENTION: BOLYPEPTIDES
    FILE REFERENCE: 3421.1066-001
    CURRENT APPLICATION NUMBER: 60/284,534
    PRIOR APPLICATION NUMBER: 60/284,534
    PRIOR PILING DATE: 2001-04-18
    NUMBER OF SEQ ID NOS: 200
    SOFTWARE: FastSEQ for Windows Version 4.0
    Isancour. 1.
    Isancour. 1.
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57.1%; Pred. No. 1.5e+02;
tive 3; Mismatches 0;
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                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sato, Aaron K.
APPLICANT: Dawson, Bruce M.
TITLE OF INVENTION: PROTEIN ANALYSIS
TITLE OF INVENTION: PROTEIN ANALYSIS
CURRENT APPLICATION NUMBER: US/10/462, 262
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: US 60/388, 642
PRIOR PILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 430
SOFTWARE: FREESEQ FOR WINDOWS VERSION 4.0
                     LOCATION: (5)..(7)
OTHER INFORMATION: X is any amino acid
                                                                 NAME/KEY: SITE
COCATION: (9)...(9)
COTHER INFORMATION: X is any amino acid
US-10-046-922-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 297, Application US/10462262 Publication No. US20040009534A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 57.1
A; Conservative
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US-10-125-869A-73
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LENGTH: 13
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Sequence 476, Application US/10280066

Sequence 476, Application US/10280066

Publication No. US20030180718A1

GENERAL INFORMATION:
APPLICANT: Pillutla, Renuka C.
APPLICANT: Spruyt, Michael
APPLICANT: Blume, Arthur J.
APPLICANT: Dedova, Olga
APPLICANT: Dedova, Olga
APPLICANT: Goldstein, Nail I.
TILLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BINDE
FILE REFERENCE: 2598-4009US1
CURRENT APPLICATION NUMBER: US/10/280,066
CURRENT APPLICATION NUMBER: US/10-24
PRIOR FILING DATE: 2001-10-24
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APPLICANT: Henzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPRENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT PILING DATE: 2001-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-36
PRIOR FILING DATE: 2000-06-36
PRIOR FILING DATE: 2000-08-36
PRIOR FILING DATE: 2000-08-03
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                                                                                                                                                              Indels
; OTHER INFORMATION: immunoglobulin binding polypeptide US-10-462-262-297
                                                                                               100.0%; Score 38; DB 15;
57.1%; Pred. No. 1.5e+02;
iive 3; Mismatches 0;
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Avail, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 287762
LENGTH: 47
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ORGANISM: Homo sapiens
PRATURE:
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BOULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
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                                       FRIOR FILLING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/USO1/00664

PRIOR APPLICATION NUMBER: PCT/USO1/00664

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/USO1/00668

PRIOR PELING DATE: 2001-01-30

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 2001-01-20

NUMBER OF SEQ ID NOS: 49117

SEQ ID NO 40409

I PRIOR PILING DATE: 2001-01-20

NUMBER OF SEQ ID NO 40409
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Pred. No. 3.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 57.1%; Ratches 4; Conservative 3;
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25 GYWQLHW 31
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US-10-425-115-287762
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-06-03
PRIOR PLING DATE: 2000-08-03
PRIOR PLING DATE: 2000-08-03
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.97

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.94

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.91

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.91
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/774,203
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; Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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17 GYWQLHW 23
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SEQ ID NO 35127
LENGTH: 29
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Publication No. US20040214272A1
RAPPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Vongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 324628
LENGTH: 61
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100.0%; Score 38; DB 17; Length 61;
Best Local Similarity 57.1%; Pred. No. 5.48+02;
Matches 4; Conservative 3; Mismatches 0; Indels
h
Similarity 57.1%; Pred. No. 5.1e+02;
4; Conservative 3; Mismatches 0: Indela
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US-10-425-115-324628
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Job time : 70.56 secs
         Query Match
Best Local Similarity
Matches 4; Conserva
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49 GYWGASW 55
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41 GYWQKQW 47
                                                                                                       1 GYWXXXW 7
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US-10-425-115-324628
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE SEFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 170197
LENGTH: 57
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| Publication No. US20040214272A1
| General Information:
| APPLICANT: La Rosa, Thomas J.
| APPLICANT: Kovalic, David K.
| APPLICANT: APPLICANT: Abou, Yihua
| APPLICANT: APPLICANT: Abou, Yihua
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| CURRENT APPLICATION NUMBER: US/10/425,115
| CURRENT APPLICATION NUMBER: US/10/425,115
| CURRENT FILING DATE: 2003-04-28
| NUMBER OF SEQ ID NOS: 369326
| LENGTH: 58
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                                                                                                                               Length 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Clone ID: PAT_MRT4530_68546C.1.pep
         ; ORGANISM: Zea may9
; FEATURE:
. OTHER INFORMATION: Clone ID: MRT4577_25533C.1.pep
US-10-425-115-287762
                                                                                                                           Query Match
100.0%; Score 38; DB 17;
Best Local Similarity 57.1%; Pred. No. 4.3e+02;
Matches 4; Conservative 3; Mismatches 0;
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; OTHER INFORMATION: Clone ID: MRT4577_44726C.1.pep
US-10-425-115-308836
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 170197, Application US/10437963;
Publication No. US2004012334341
GENERAL INFORMATION:
APPLICANT: A ROSS THOUS A
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Bradzuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                   40 GYWTIFW 46
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19 GYWLFMW 25
                                                                                                                                                                                                                        1 GYWXXXW 7
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ORGANISM: Zea mays
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US-10-425-115-308836
                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-10-437-963-170197
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                  Copyright
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protein search, using sw model • OM protein January 3, 2005, 16:20:13; Search time 15:68 Seconds (without alignments) 42.954 Million cell updates/sec Run on:

US-10-046-922-67 1 GYWXXXW 7 Perfect score: Sequence: Title:

ALOSUM62DX Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* . . . . Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ				
Result		Query				
No.	Score	Match	Length	8	QI	Description
1	38	100.0	71	7	\$22905	lysis protein S -
7	38	100.0	72	N	T03190	
е	38	100.0	83	~	E69903	
4	38	100.0	108	~	S12193	
2	38	100.0	142	N	C34903	•~
y	38	100.0	187	~	G83047	ď
7	38	100.0	~	~	S76385	
80	38	100.0	218	~	D87264	
6	38	100.0	227	N	S73905	υ
10	38	100.0	250	7	A69843	hypothetical prote
11	38	100.0	254	~	F82733	<b>LRNA</b>
12	38	100.0	257	~	E75325	probable mccF prot
13	38	100.0	261	N	JC5806	- 8 1
14	38	100.0	263	N	JC5622	aquaporin 8 - rat
15	38	100.0		~	F83188	phosphatidate cyti
16	38	100.0		~	JC4832	
17	38	100.0		0	E95268	probable ABC trans
18	38	100.0		~	AB2307	hypothetical prote
19	38		282	N	H95869	
20	38	100.0	286	7	E88690	protein F41H10.7 [
21	38	100.0	289	7	G72215	~ •
22	38	100.0	٣	~	C83886	
23	38	100.0	m	~	C82611	hypothetical prote
24	38	100.0	345	~	T37139	_
25	38	100.0	360	N	AE2047	
26	38	100.0	421	~	D82500	cal
27	38		441	~	C95307	probable transport
28	38	100.0	447	~	H97146	siderophore/Surfac
29	38	100.0	448	~	AB0301	conserved hypothet

probable secreted ABC transporter (a probable amino aci arginine/ornithine arginine/ornithine	arginine/crnitine probable ABC trans hypothetical prote oligopeptide trans	probable carbohydr hypothetical prote probable dipeptide probable ABC trans	hypothetical prote hypothetical prote
T35164 D70048 E83497 T46745 JH0110	G86878 G86878 C95282 AI3201 S77572	E83268 T15414 B95952 G95389	AC2392 AH2975
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1000.0 1000.0 1000.0	00000	1000.0	100.0
888888		38 38 38	38
333 333 344 344		4 4 4 4 0 4 5 6	44 45

#### ALIGNMENTS

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C. Accession: S22905
R. Bonovich, M.T.; Young, R.
J. Bacterariol. 137, 2897-2905, 1991
A.Title: Dual start motif in two lambdoid S genes unrelated to lambda S.
A.Tatle: Dual start motif in two lambdoid S genes unrelated to lambda S.
A.Accession: S22905
A.Aocession: S22905
A.Aocession: S22905
A.Aocession: S22905
A.Aocession: B22905
A.Aocession: S22905
A.Aocession: S22905
A.Aocession: DNA
A.Residues: 1-71 cBON>
A.Gorder-references: EMBL:M65239; NID:g215466; PIDN:AAA32349.1; PID:g215467
A.Gorder-references: EMBL:M65239; NID:g215466; PIDN:AAA32349.1; PID:g215467
C. Genetics: S
C. Keywords: alternative initiators; cell wall lysis; transmembrane protein F7:17/Product: lysis protein inhibitor S107 #status predicted cMAT1>
F:A-71/Product: lysis protein S105 #status predicted cMAT2>
F:A-28/Domain: transmembrane #status predicted cTM1>
F:36-58/Domain: transmembrane #status predicted cTM2>
                                               C;Species: phage 21
C;Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 08-Oct-1999
lysis protein S - phage 21
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Gaps ö DB 2; Length 71; 0; Indels h 100.0%; Score 38; DE Similarity 57.1%; Pred. No. 52; 4; Conservative 3; Mismatches Query Match Best Local Similarity Matches 4; Conserva

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[||:::| 21 GYWFLQW 27 1 GYWXXXW 7 δ 셤

Pypothetical protein 72B - rice mitochondrion C; Species: mitochondrion Oryza sativa (rice)
C; Species: Tollso
B; Itadani, H.; Wakasugi, T.; Sugita, M.; Sugiura, M.; Nakazono, M.; Hirai, A.
Plant Cell Physiol. 35, 1239-1244, 1994
A; Title: Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA: the existence
A; Title: Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA: the existence
A; Reference number: Z14841; MUID:95211382; PMID:7545979
A; Reference number: Z14841; MUID:95211382; PMID:7545979
A; Residues: 1-72 citA>
A; Residues: 1-72 citA>
A; Residues: 1-72 citA>
A; Residues: Lora citivar Nipponbare
C; Genetics:
A; Experimental source: cultivar Nipponbare
C; Genetics:
A; Genome: mitochondrion

Query Match

C; Keywords: mitochondrion

100.0%; Score 38; DB 2; Length 72;

us-10-046-922-67.dx.rpr

Best Local Similarity

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Gispecies: Mus musculus (house mouse)
Cispecies: Musculus (house mouse)
Cispecies: Musculus (house mouse)
Cispecies: Musculus (house)
Cisp
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CiSpecies: Pseudomonas aeruginosa
CiSpecies: Pseudomonas aeruginosa
CiDate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
CiAccession: G83.04.
CiAccession: G83.04.
CiAccession: C8.1; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Briadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83047
A;Accession: G83047
A;Accession: C83047
A;Residues: 1-187 < STOX
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A;Experimental source: strain PAO1
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R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 1.2e+02;
3; Mismatches 0; Indels
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A;Accession: S76385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.1%; Pred. No. 97; ive 3; Mismatches
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57.1%; P
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nes 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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126 GYWFAYW 132
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                                                                      RESULT 5
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C;Species: Bacillus subtils
C;Species: Bacillus subtils
C;Decies: Bacillus
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C;Decies: Bacillus
C;Decies: Bacillus
C;Escon, C;Escon, C;Escon, C;Cildwell, B;Capuano, V;Carter, N.M.; Chc
C;Escon, C;Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Poulger, D; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
A;Authors: Poulger, D; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
Koetter, P.; Koningstein, G; Krogh, S.; Kumtan, M.; Kuitta, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S. M.; Levine, A.; Liu, H.; Mauda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Saddie, Y.; Sato, T.; Sacon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sakiguchi, J.; Sakowska, A.; Gauchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Voshida, R.; Vittle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Althors: Voshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
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C; Genetics:
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R;Drolet, M.; Zanga, P.; Lau, P.C.K.
Mol. Microbiol. 4, 1381-1391, 1990
A;Title: The mobilization and origin of transfer regions of a Thiobacillus ferrooxidans
A;Reference number: S12188; MUID:91125140; PMID:2280689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: E69903
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-83 < KUN>
A; Cross-references: UNIPROT: 034654; GB: Z99114; GB: AL009126; NID: g2634230; PIDN: CAB13852.
A; Experimental source: strain 168
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C;Species: Thiobacillus ferrooxidans
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S12193
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Pred. No. 52;
3; Mismatches
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57.1%; Pred. No. 60;
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A,Status: preliminary; translation not shown
                                   4; Conservative
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Ristperimental source: strain 9a5c
Ristmpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H sa-Neco, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre, Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Martins, E. A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
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C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change .09-Jul-2004
C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change .09-Jul-2004
C; Accession. B8726 # R. T. Feldblyum, T. V.; Paulsen, I. T.; Nelson, K. E.; Bisen, J.; Heidelberg, J. B.; Laub, M. T.; DeBoy, R. T.; Dodson, R. J.; Durkin, A. S.; Gwinn, M. L.; Haft, D. H.; Kolon h. J.; Ermolaeva, M.; White, O.; Salzberg, S. L.; Shapiro, L.; Venter, J. C.; Fraser, C. M. Proc. Natl. Acad. Sci. US. A. 98, 4136-4141, 2001
A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A67249; MUID:21173698; PMID:11259647
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A;Cross-references: UNIPROT:Q9ABU5; GB:AE005673; NID:g13421234; PIDN:AAK22112.1; GSPDB:C
C;Genetics:
A;Gene: CC0125
                                                                                    A;Residues: 1-218 «KAN»
A;Cross-references: UNTRROT:Q55705; EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAA1023
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: probable alkaline phosphatase yngC
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A,Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
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Pred. No. 1.4e+02;
3; Mismatches 0; Indels
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D87264
hypothetical protein CC0125 [imported] - Caulobacter crescentus
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Matches 4; Conservative
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139 GYWRPAW 145
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C,Superfamily: CDPdiacy]
C,Keywords: transferase
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A; Status: preliminary
Status: preliminary
                                                 A; Molecule type: DNA
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Cipacesion: A69843

Rikunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterk C.; Bron, S.; Broullet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chol A.; Ellich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 190, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fuita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerk ich, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kuita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T. M.; Portetelle, Y.; Alloris, C.; Roche, E.; Rosch, M.; Sadale, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Winters, Y.; Voshida, K.; Yasta, T.; Yasta, K.; Yasta, K.; Yasta, K.; Yasta, K
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A;Experimental source: strain 168
C;Genetics:
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: F82733
F;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Feference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
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A, Molecule type: DDA
A, Reaidues: 1-254 «SIM»
A, Cross-references: UNIPROT: Q9PELO; GB: AE003939; GB: AE003849; NID: g9105949; PIDN: AAF83828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Bacillus subtilis
;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein yjbA - Bacillus subtilis
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185 GYWYTEW 191
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84 GYWARKW 90
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1 GYWXXXW
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Search completed: January 3, 2005, 16:34:52
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     222 GYWDFHW 228
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nes 4; Conserv
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-271 <STO>
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Matches 4
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A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Recidues: 1-257 <WHL>
A;Cross-references: UNIPROT:Q9RSX1; GB:AE002038; GB:AE000513; NID:g6459790; PIDN:AAF1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Ma, T.; Yang, B.; Verkman, A.S.
Biochem. Blophya. Res. Commun. 240, 324-328, 1997
A;Title: Cloning of a novel water and urea-permeable aquaporin from mouse expressed strc
A;Reference number: JC5806; MUID:98049830; PMID:9388476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: mRNA
A;Residues: 1-261 <MAA.>
A;Cross-references: UNIPROT:P56404; DDBJ:AF018952; NID:g2153796; PIDN:AAB68847.1; PID:g2
C;Comment: This protein functions as a mercurial-sensitive water channel.
C;Superfamily: lens fiber membrane major intrinsic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                          probable mccF protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O9-Jul-2004
C;Accession: E75325
R;White, O; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 26, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
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C;Date: 27-Jan.1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Accession: JC5806
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F;92-94/Region: NPA motif
F;210-212/Region: NPA motif
F;85,139/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                         100.0%; Score 38; DB 2; Length 254; 57.1%; Pred. No. 1.6e+02; ive 3; Mismatches 0; Indels
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Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels
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3; Mismatches
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Best Local Similarity 57.1.
4; Conservative
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171 GYWLRNW 177
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GYWPDRW 28
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1 GYWXXXW 7

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aquaporin 8 - rat

aquaporin 8 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004

C;Date: 09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004

C;Date: 09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004

R;Ishibashi, K.; Kuwahara, M.; Kageyama, Y.; Tohsaka, A.; Marumo, F.; Sasaki, S.

Biochem. Biophys. Res. Commun. 237, 714-718, 1997

A;Ritle: Cloning and functional expression of a second new aquaporin abundantly expressed

A;Reference number: JC5622; MUID:97445104; PMID:9299432

A;Reference number: JC5622, MUID:97445104; PMID:9299432

A;Residues: 1-263 «ISH>

A;Residues: 1-264 «ISH>

A;Residues: 1-264 «ISH>

A;Residues: 1-263 «ISH>

A;Residues: 1-264 «ISH>

A;Residues: 1-260 «IS
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: F83188
C;Stover; C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Brisadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A;Reference number: A82950; MUID:20437337; PMID:10984043
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A,Experimental source: strain PAO1
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57.1%; Pred. No. 1.7e+02;
tive 3; Mismatches 0;
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SEQUENCE FROM N.A. STRAIN=H.I.8.;
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P2736 bacteriopha
Q76210 shigella fl
Q9fcw3 escherichia fl
Q93ml2 shigella fl
Q83ml2 shigella fl
Q83ml2 shigella fl
Q83570 oryza sativ
Q34654 bacillus su
Q35505 drosophila
Q61114 drosophila
Q61114 drosophila
Q2188 thiobacillu
Q728a6 desulfovibr
Aas97170 desulfovibr
Aas97509 desulfovibr
Aas95609 desulfovibr
Q707v6 syncehococc
Q8mk57 bos taurus
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Cae50615 corynebac
Q9hv15 pseudomonas
Q780ps bordetella
Q7w3f9 bordetella
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bordetella
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                                                      (without alignments)
47.317 Million cell updates/sec
                                               January 3, 2005, 16:12:00 ; Search time 85.12 Seconds
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Q7vbg3
Q7tuv7
      GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                           1825181 segs, 575374646 residues
                                                                                                                                                                                                                                                               SUMMARIES
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VLYS BPP21
O7C230
097C230
098823
083852
083853
095805
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001114
VML2 THIFE
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AAS97170
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071706
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Maximum Match 100%
Listing first 45 summaries
                                 OM protein - protein search, using sw model
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Q7W0P5
Q7W3P9
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Q7WL18
Q9KY37
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2: uniprot trembl:*
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Maximum DB seq length: 2000000000
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Match Length DB
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            Q55705 synechocyst
Q7vzm7 bordetella
Q9abus caulobacter
Q98486 zea mays (m
P75520 mycoplasma
Q72kr5 thermus the
Aa880801 thermus t
Q7w7n0 bordetella
Q9wgw9 human immun
Q8ggG1 arabidopsis
Q31597 bacillus su
Q31597 bacillus su
bacteroides
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X MEDLINE=2457T;

X MEDLINE=2250274; PubMed=12704152;

X MEDLINE=2250274; PubMed=12704152;

X MEDLINE=2520274; PubMed=12704152;

X Med S., Goldberg M. B., Burland V., Venkatesan M.M., Dang W.,

X Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,

X Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,

X Schwartz D.C., Blattner R.R.,

R Schwartz D.C., Blattner R.R.,

R Schwartz D.C., Blattner R.R.,

RT Flexneri serocype 2a strain 2457T.";

RL Infect. Immun. 71:2775-2786(2003).

R EMBL; AG016980; Applis 13:1;

DR EMBL; AG016980; Applis S.,

InterPro; IPR007064; Lysis S.,

R Hypothetical protein.

KW Hypothetical protein.
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Q7UDB7;
01-OCT-2003 (TERMBLrel. 25, Last sequence update)
01-OCT-2003 (TERMBLrel. 25, Last sequence update)
01-MAR-2004 (TERMBLrel. 26, Last annotation update)
Hypothetical bacteriophage protein.
Name-ybcR; OrderedLocusNames=S0714;
Shigella flexneri.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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Enterobacteriaceae, Escherichia
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PGSA MYCPN
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Q7VZM7
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031597
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GYWFLQW 27
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Best Local Similarity
Matches 4; Conserv
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Shigella.
NCBI_TaxID=623;
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Best Local Similarity 57.1.
Best Local 4; Conservative
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21 GYWFLQW 27
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Shigella flexneri.
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MEDLINE=91210180; PubMed=2019562;
BONOVICH M.T., Young R.;
"Dual start morif in two lambdoid S genes unrelated to lambda S.";
J. Bacteriol. 173:2897-2905(1991).
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
                        Unkmeir A., Schmidt H.,
"Structural analysis of phage-borne stx genes and their flanking
sequences in shiga toxin-producing Escherichia coli and Shigella
dysenteeriae type 1 strains.";
Infect. Immun. 68:4856-4864(2000).
BMBL; AJ271139; CAC05573.1;
InterPro; IPR007054; Lysis...S.
Pfam; PF04971; Lysis...S.
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Pfam; PF04971; Lysis_S; 1.
Phage lysis protein.
PSEQUENCE 71 AA; 7893 MW; 8690A8F25234A3E2 CRC64;
                                                                                                                                                                                                                                                                                                 49 AA; 5227 MW; 0B6914DD9AE25E00 CRC64;
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01-AUG-1992 (Rel. 23, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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      MEDLINE=20407286; PubMed=10948097;
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Best Local Similarity 57.1%;
Matches 4; Conservative
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
07-JUL-2004 (TrEMBLrel. 27,
07-JUL-2004 (TrEMBLrel. 27,
07-JUL-2004 (TrEMBLrel. 27,
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es 4; Conservative
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21 GYWFLQW 27
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P27360;
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SEQUENCE
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Q7C2J0;
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VIYS. BPP21
VIYS. BPP21
DT 01-AUG
DT 01-AUG
DT 05-UUL
DE LYSIS
GN Bacter
CC VITUS
CC Lambda
OX VITUS
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Schmidt H., Scheef J., Morabito S., Caprioli A., Wieler L., Karch H.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ270998; CAC05565.1;
InterPro; IPR007054; Lysis_S.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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100.0%; Score 38; DB 2; Length 71; 57.1%; Pred. No. 3.7e+02; ive 3; Mismatches 0; Indels
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 71 AA; 7923 MW; 9B4D68F25220B7E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                               71 AA.
                                                                                                                                                                                                                                                                                                                                  PRT;
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MEDLINE=20407286; PubMed=10948097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nfect. Immun. 68:4856-4864(2000).
                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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RESULT 6

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"Structure of long and short copies of the mobile dispersed gene MDG3 of Drosophila melanogaster."; Dokl. Akad. Nauk SSSR 282:1483-1486(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN=301 / Serotype 2a;

MEDLINE=22272406; PubMed=12384590;

Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,

Jin O., Yuang F., Zhang Y., Zhang J., Yang G., Wu H., Qu D., Dong J.,

Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,

Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Protecbacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
NCBI_TaxID=623;
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MEDLINE-95308541; PubMed=7788722;
Nakazono M., Itadani H., Wakasugi T., Tsutsumi N., Sugiura M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 38; DB 2; Length 71; 57.1%; Pred. No. 3.7e+02; tive 3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                Last annotation update)
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4; Conservative
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OrderedLocusNames=SF0689;
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21 GYWFLQW 27
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1 GYWXXXW 7
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                                                                                                                                                                                                                                  01-JUN-2003
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01-OCT-2003
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Matches
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MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Kang G., Wu H., Qu D., Dong J.
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Shigella.
                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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InterPro; IPR007054; Lysis_S.
Pfam; PF04971; Lysis_S; 1.
                                                                                               01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
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Matches 4; Conservative
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                                                                                                                                                                                                         OrderedLocusNames=S0231;
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                                                   PRELIMINARY;
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21 GYWFLOW 27
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Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
A Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Britan K.-D., Errington J., Fabret C., Ferrari B., Foulger D.,
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Rinsoppi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
Klein C., Kobayashi Y., Koetter P., Koningstein G., Eruber J.,
Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
Medigue C., Medina N., Mellado R.P., Misuno M., Moestl D., Nakai S.,
A Noback M., Noone D., O'Really M., Ogawa K., Ogiwara A., Oudega B.,
A Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
                                    SEQUENCE FROM N.A.
MEDLINE=95211382; PubMed=7545979;
MEDLINE=95211382; PubMed=7545979;
MEDLINE=95211382; PubMed=7545979;
Micleotide sequence of a 28-kbp portion of rice mitochondrial DNA:
the existence of many sequences that correspond to parts of
mitochondrial genes in intergenic regions.";
Plant Cell Physiol. 35:1239-1244(1994).
EMBL; D32052; BAA06811.1;
PR; T03190; T03190.
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Wambutt R., Wedler H., Lapidus A., Sorokin A., Ehrlich S.D.;

"Sequence analysis of the Bacillus subtilis chromosome region between
the odhAB and sspc loci cloned in a yeast artificial chromosome.";

Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein yodI.
Name=yodI; Synonyms=yolA; OrderedLocusNames=BSU19610;
                                                                                                                                                                                                             72 AA; 8155 MW; D42DE53BED28432E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                 83 AA
transcribed from alternative promoters.";
                                                                                                                                                                Gramene, Q35302; -. GO: GO: 0005739; C:mitochondrion; IEA.
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10-OCT-2003 (Rel. 42, Last seq
             Curr. Genet. 27:184-189(1995)
                                                                                                                                                                                                                                                    Best Local Similarity 57.1
Matches 4; Conservative
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SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose B., Sacholar V., Sato T., Scanlan B., Schleich S., Schroeter R., Scoffene F., Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A., The complete genome sequence of the Gram-positive bacterium Bacillus
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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57.1%; Pred. No. 4.2e+02;
ive 3; Mismatches 0; Indels
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57.1%; Pred. No. 4.5e+02;
ive 3; Mismatches 0; Indels
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PIR, E69903; E69903.
Subcitiet; BG13537; yodl.
InterPro; IPR008991; Trans1 SH3_like.
Complete proteome; Hypothetical protein; Transmembrane.
TRANSMEM
SB 00
Potential.
SEQUENCE 83 AA; 9194 MW; 99F58EA2F0F36A43 CRC64;
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Best Local Similarity 57.11
احد جمير 4; Conservative
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QGIIL4;

RESULT 12
061114
AC 061116
DT 065-JU
DT 055-JU

Q6IIL4

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SEQUENCE FROM N.A.

Pubmed=15077118; DOI=10.1038/nbt959;
Rubed=15077118; DOI=10.1038/nbt959;
Reidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
A. Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
A. Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
A. Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
A. Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
A. Dimitroy G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
A. Peldblyum T.V., Wall J.D., Voordown G., Fraser C.M.;
The genome sequence of the anaerobic, sulfate-reducing bacterium
Desulfovibrio vulgaris Hildenborough.";
Nat. Biotechnol. 22:554-559(2004).
R. Bibl., AB017318; AAS97170.1; -.
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Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T., Kolonay J.F., Eisen J.A., Ward N., Methe B.A., Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R., Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio.
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                                                                                                                                                                                                                                                                                                                                                                                    Lipoprotein, putative.
OrderedLocusNames=DVUZ698;
Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
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                                        Length 108;
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57.1%; Pred. No. 5.9e+02;
tive 3; Mismatches 0; Indels
                                                                              0; Indels
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SEQUENCE 120 AA; 13418 MW; CD3581657D76E183 CRC64;
108 AA; 12335 MW; A8E67717C109A57E CRC64;
                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                        100.0%; Score 38; DB 1; 57.1%; Pred. No. 5.3e+02;
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(TrEMBLrel. 27, L
(TrEMBLrel. 27, L
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                                                                                   Conservative
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               Query Match
Best Local Similarity
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89 GYWRSSW 95
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54 GYWIDRW 60
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26-APR-2004 (
11-MAY-2004 (
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05-JUL-2004
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SEQUENCE
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AAS97170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Hild M., Beckmann B., Haas S., Koch B., Solovyev V., Busold C., Fellenberg K., Boutros M., Vingron M., Sauer F., Hoheisel J., Paro R., "An integrated gene annotation and transcriptional profiling approach towards the full gene content of the Drosophila genome."; Genome Biol. 5:R3-R3(2003).

-i- MISCELLANBOUG: The sequence shown here is derived from an EMBL/Genbank/DDBJ third party annotation (TPA) entry.

EMBL; BK003052; DAA032222.1; ...
SEQUENCE 102 AA; 11777 MW; CD4044EC9325CF46 CRC64;
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"The mobilization and oxigin of transfer regions of a Thiobacillus
ferrooxidans plasmid: relatedness to plasmids RSF1010 and pSC101.";
Mol. Microbiol. 4:1381-1391(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillales; Acidithiobacillaceae; Acidithiobacillus.
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                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).

Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

NCBI_TaxID=7227,
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypotherical 12.3 kDa protein in mobb 3'region (ORF 4).
Thiobacillus ferrooxidans.
                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Pred. No. 5.1e+02;
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57.1%; Pred. No. 5...
3; Mismatches
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PIR; S12193; S12193.
Hypothetical protein; Plasmid.
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73 GYWIQEW 79
                      GYWQCNW 76
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SEQUENCE FROM N.A.
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DS PLOST
DE HYPOCTY
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DS PLOST
OC Bacteric
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Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D.,
Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
Peldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
The genome sequence of the anaerobic, sulfate-reducing bacterium
Desulfovibrio vulgaris Hildenborough.";
Nat. Biotechnol. 22:554-559(2004).
FMBL, AE017318, AAS97170.1; -.
Lipoprotein.
SEQUENCE 120 AA; 13418 MW; CD3581657D76E183 CRC64;
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0
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Search completed: January 3, 2005, 16:32:33 Job time : 88.12 secs

1 GYWXXXW 7 | | | | ::: | 54 GYWIDRW 60

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

January 3, 2005, 17:00:47; Search time 146 Seconds (without alignments) 17.199 Million cell updates/sec Run on:

US-10-046-922-67 38 1 GYWXXXW 7 Scoring table: score: Sequence: Perfect

2002273 seqs, 358729299 residues <BLOSUM62DX ⁴
Gapop 10.0 , Gapext 0.5</pre> Searched:

116873 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s: geneseqp2000s: geneseqp2001s: geneseqp2001s: geneseqp2002s: geneseqp2003bs: geneseqp2003bs: A_Geneseq_23Sep04:* .......... Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	Aay76794 Somatosta	Abp53964 VEGFR-3 b		_	Aau83934 Tyrosine	Aar08140 Neurokini	Aay76792 Somatosta		Adj25834 Tyrosine		Aar46290 PTP-D1/D2	Aaw43021 Protein t	Aay81787 Protein t	Aar62543 Fibronect	Aay14751 Tyrosine	•	Aay33139 Rabbit ca	Aaw28937 Opioid pe		Aay23046 Opioid pe		Abg75386 C melo se	Aaw40924 Leader se	Aay16913 Heat shoc	Aay16925 Heat shoc
ID	AAY76794	ABP53964	ABP53418	AAR93713	AAU83934	AAR08140	AAY76792	ABP53416	ADJ25834	AAR48807	AAR46290	AAW43021	AAY81787	AAR62543	AAY14751	AAY14752	AAY33139	AAW28937	AAR93795	AAY23046	AAG78945	ABG75386	AAW40924	AAY16913	AAY16925
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* Query Match	100.0	100.0	100.0	84.2					_	•					73.7				71.1	71.1	71.1	71.1	71.1	71.1	71.1
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7 3 AAY76793 7 3 AAU78246 7 3 AAU77087	7 4 AAU72055 7 4 AAU72067 7 5 AAU80617 7 5 AAU80605	7 S AAU81571 7 S ABP53417 7 S AAU70373	7 6 ABU79853 7 6 AAO26659 7 7 ADG72569	7 7 ADG72581 7 7 ADG72777 7 7 ADG72789	7 7 ADL17115 7 7 ADL17125 5 2 AAR76079 5 3 AAY32257
27 71.1 27 71.1 27 71.1	27 71.1 27 71.1 27 71.1 27 71.1	27 71.1 27 71.1 27 71.1	27 71.1 27 71.1 27 71.1	27 71.1 27 71.1 27 71.1	27 71.1 27 71.1 26 68.4 26 68.4
26 27 28	9 9 9 8 9 1 9 9	3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	38 38 38	4 4 3 1 0 0	4 4 4 4 2 6 4 8

### ALIGNMENTS

Somatostatin analogue; therapy; cyclic peptide; autoimmune disease; endocrine disorder; cancer; diabetic-associated complication; diagnosis; gastrointestinal disorder; inflammatory disease; pancreatitis; atherosclerosis; restenosis; post-aurgical pain; VIP secretion inhibitor; hormone-secreting tumour; hormone-dependent tumour; diarrhoea; vasoactive intestinal peptide; non-insulin dependent diabetes mellitus. Somatostatin analogue peptide 3181. AAY76794 standard; peptide; 7 AA. (first entry) 20-APR-2000 AAY76794; RESULT 1 

/note= "D-form residue" Location/Qualifiers /note= "Trp-NH2" Misc-difference Modified-site Synthetic.

99WO-IL000329. 98US-00100360. 98US-00203389. 15-JUN-1999; WO9965508-A1 19-JUN-1998; 02-DEC-1998; 23-DEC-1999.

Gellerman G; Afargan MM, Hornik V,

(PEPT-) PEPTOR LTD.

WPI; 2000-136888/12.

Cyclized somatostatin analogs for inhibiting growth hormone secretion from anterior pituitary and as antiproliferative agents for the treatment of tumors.

Example 11; Page 61; 82pp; English.

This sequence represents a somatostatin analogue of the invention. The invention relates to a backbone cyclised somatostatin analogue that has

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                                                                                                                                                                                                           analogues can be used for the treatment patients with hormone-secreting and hormone-dependent tumours. They reduce diarrhoea through the inhibition of vasoactive intestinal peptide (VIP) secretion and by direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
one building unit containing a nitrogen atom of the peptide backbone connected to a bridging group comprising an amide, thioether, thioester or disulphide. At least one building unit is connected via a bridging group to form a cyclic structure with a moiety selected from a second building unit, side chain of or N-terminal amino acid residue. A composition containing the analogue may be used for preventing disorders such as cancers, autoimmune diseases, endocrine disorders, diabetic diseases, pencreatis, atherosclerosis, restenosis and post-surgical pain. It may also be used for diagnosing cancer. The backbone cyclic analogue is used for imaging the existence of metastases. Somatostatin
                                                                                                                                                                                                                                                                effect on intestinal secretion. Somatostatin analogues selective to type 2 and 5 receptors may be used for treatment of non-insulin dependent diabetes mellitus. They are useful for the prevention of atherosclerosis and restenosis. The analogues are metabolically stable, selective in their in-vivo activities and safe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
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0
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/note= "X is any amino acid"
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Best Local Similarity
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1 GYWKVCW
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ABP53964
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The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, puncress, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic; somatotropin release inhibiting factor; somatostatin receptor subtype; synthesis; antiarteriosclerotic; immunosuppressive; cytostatic; cancer; antidiabetic; antiinflammatory; somatostatin receptor ligand; atherosclerosis; autoimmune disease; diabetic-associated complication; endocrine disorder; inflammation; gastrointestinal disorder; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Backbone cyclised somatostatin analogue PTR 3181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 38; DB 5; I 100.0%; Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (fluorenylmethoxycarbonyl)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gellerman G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                 Claim 21; Page 81; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP53418 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pancreatitis; post-surgical pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-00100360.
98US-00203389.
99WO-IL000329.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HORN/) HORNIK V.
(AFAR/) AFARGAN M M.
(GELL/) GELLERMAN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GYWXXXW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYWXXXW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7 AA;
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Modified-site
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15-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Gaps

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Owen TJ, Kudlacz EM, Buck SH, Harbeson SL;
                                Example 12; Page 21; 30pp; English
                                                                                                                                                                                                                                                  Cyclo[-Tyr-trp-Leu-Arg-Gly-Trp-].
                                                                                                                                                                                                                  AAR93713 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                         (RICH ) MERRELL DOW PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                    95WO-US000296
                                                                                                                                                                                                                                                                                                                                                                               94US-00191571,
                                                                                                                                 from the present invention
                                                                                                                                                                                                                                       10-MAY-1996 (first entry)
                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                              /note= '
Tyr(1) t
     WPI; 2002-681319/73
                                                                                                                                                           Best Local Similarity
                                                                                                                                                                            GYWXXXW 7
                                                                                                                                                                                                                                                                   analgesic; cyclic.
                                                                                                                                                                                  GYWKVCW .
                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                           Sequence 7 AA;
                                                                                                                                                                                                                                                                                        Key
Modified-site
                                                                                                                                                                                                                                                                                                                        Modified-site
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                                                                                                                                                                                                                                                                                                                                                                   10-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                                         10-AUG-1995.
                                                                                                                                                                                                                                                                             Synthetic
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The method relates to a method of identifying a modulator of cell growth, comprising assessing and comparing the activities of site-specific DNA recombinase (I) or type I DNA topolsomerase (II) in presence and absence of a test substance. A difference in activity of (I) and (II) assessed in the presence and absence of the test substance indicates that the test substance modulates cell growth. The identified cell growth modulator, preferably an inhibitor of (I) or (II), is useful for inhibiting cell growth in a subject, preferably a human. The inhibitor inhibits (I) which having or suspected of having tumour or cancer, where the method further involves administering an effective of antitumour or anticancer agent or
                                                               peptide derivs. - are neurokinin A and tachykinin antagonists for treating asthma or as analgesics.
                                                                                                                                                                                 The patent describes novel cyclic hexapeptide and octapeptide compounds which are antagonists of neurokinin A and which are useful medically as analgesics and for treating respiratory diseases such as athma. The present sequence represents a specifically preferred example of the new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tyrosine recombinase; antibacterial; cytostatic; cell growth modulator; site-specific DNA recombinase; type I DNA topoisomerase; tumour; tyrosine recombinase; cancer; Holliday junction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying cell growth modulators for inhibiting cancer cell growth in humans, involves assessing and comparing activity of site-specific recombinase or type I DNA topoisomerase in presence/absence of test
                                                                                                                                                                                                                                                                                                                                                                     84.2%; Score 32; DB 2; Length 6; larity 50.0%; Pred. No. 1.7e+06; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tyrosine recombinase inhibitory peptide #37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 39; Page 90; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU83934 standard; peptide; 6 AA
                                                                                                                                     Claim 8; Page 69; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUN-2001; 2001WO-US020046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUN-2000; 2000US-00602087.
                                                                 New cyclic peptide derivs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Segall A, Pinilla C;
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
3, Conserve
                     WPI; 1995-336695/43
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1 YWLRGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 YWXXXW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200198540-A2.
                                                                                                                                                                                                                                                                                                                         Sequence 6 AA;
                                                                                            e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   substance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU83934;
                                                                                                                                                                                                                                                                                peptides
                                                                                         useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU83934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                     The present invention describes backbone cyclised somatostatin analogues (I) that incorporates at least one building unit containing one nitrogen atom of the peptide backbone connected to a bridging group (comprising an amide, thiotether, thioester or disulfide) where at least one building unit is connected via the bridging group to form a cyclic structure with a moiety selected from the group consisting of a second building unit, the side chain of an amino acid residue of the sequence or the N-terminal amino acid residue. (I) has antiatteriosclerotic, immunosuppressive,
                                                                                                                                                                                                                                                                                                                                                                                                                                  associated complications, endocrine disorders, inflammation, gastrointestinal disorders, pancreatitis, post-surgical pain, and restenosis. (I) can also be used in the disgnosis of cancer, by imaging the existence of mecastases, it being labeled with a detectable probe. The present sequence represents a backbone cyclised somatostatin analogue
                                                                                                                                                                                                                                                                                                                                                                cytostatic, antidiabetic, antiinflammatory and analgesic activities, and can be used as a somatostatin receptor ligand. (I) are useful in the treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "not an N-terminal amino acid, but condensed with {\tt Irp(6)} to form a cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "not a C-terminal amino acid, but condensed with
to form a cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurokinin A antagonist; tachykinin; respiratory disease; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                          New backbone cyclized somatostatin analogs are e.g. useful in treatment of atherosclerosis, autoimmune diseases and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 5; Length 7; Pred. No. 1.7e+06; 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "D-form residue"
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treatment; or who are, or are suspected of being infected by a bacterium, in which case the inhibitor inhibits Holliday junction intermediate resolution activity of tyrosine recombinase. The method further involves administering an effective amount of antibiotic or antibacterium treatment. AAU83898-AAU83991 represents tyrosine recombinase inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide antagonists of the NK-2-receptor of neurokinin A are useful in
the treatment of Bronchoconstrictions or spasms of the intestines or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic peptide antagonists of neurokinin A - solid phase synthesis, active against bronchoconstricting or spasm.
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Santicioli P;
                                                                                                                                    ö
                                                                                                         Score 32; DB 5; Length 6; Pred. No. 1.7e+06; 3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patacchini R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32; DB 2; I
Pred. No. 1.7e+06;
                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                        NK-2-receptor; bronchoconstriction; spasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pestellini V, Maggi CA,
                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                            AAR08140 standard; protein; 7 AA.
                                                                                                                                                                                                                                                                                                                  Neurokinin A peptide antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                              'label= D-Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                     label= D-Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= D-Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= D-Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 7; 9pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90EP-00830234.
                                                                                                         84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89IT-00009432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.2%;
50.0%;
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                                                                                                                                                                                                                                                                                          27-FEB-1991 (first entry)
                                                           peptides of the invention
                                                                                                                                    3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rovero P, Pestellin:
Giuliani S, Meli A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1990-363658/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                           Query Match
Best Local Similarity
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YWCYWW 6
                                                                                                                                                          YWXXXW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         urinary bladder
                                                                                    Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
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                                                                                                                                                                                                                                                                    AAR08140;
                                                                                                                                    Matches
                                                                                                                                                                                                                                RESULT 6
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This sequence represents a somatostatin analogue of the invention. The invention relates to a backbone cyclised somatostatin analogue that has connected to a bridging group comprising an amide, thioether, thioester or disulphide. At least one building unit is connected to a bridging group comprising an amide, thioether, thioester or disulphide. At least one building unit is connected from a second building unit, side chain of or N-terminal amino acid residue. A composition containing the analogue may be used for preventing disorders outh as cancers, autoimmune diseases, endocrine disorders, inflammatory diseases, pancreatitis, atherosclerosis, restenosis and post-surgical associated complications, gastrointestinal disorders, inflammatory diseases, pancreatitis, atherosclerosis, restenosis and post-surgical cancer and hormone-dependent tumours. They reduce diarrhoea backbone cyclic analogues can be used for the treatment patients with hormone-secreting and hormone-dependent tumours. They reduce diarrhoea through the inhibition of vasoactive intestinal peptide (VIP) secretion and by direct effect on intestinal secretion. Somatostatin analogues selective to type cancer metalitus. They are useful for the prevention of atherosclerosis and restenosis. They are useful for the prevention of atherosclerosis and restenosis. They are useful for the prevention of atherosclerosis and restenosis. They are useful for the prevention of atherosclerosis and restenosis. They are useful for the prevention of atherosclerosis
                                                                                                                                                                                                                                                                                 Somatostatin analogue; therapy; cyclic peptide; autoimmune disease; endocrine disorder; cancer; diabetic-associated complication; diagnosis; gastrointestinal disorder; inflammatory disease; panoreatitis; atherosclarosis; restenosis; post-aurgical pain; VIP secretion inhibitor; hormone-secreting tumour; hormone-dependent tumour; diarrhoea; vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyclized somatostatin analogs for inhibiting growth hormone secretion from anterior pituitary and as antiproliferative agents for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "D-form residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                             Somatostatin analogue peptide 3177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 11; Page 61; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gellerman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    their in-vivo activities and safe
                                                                                                                      AAY76792 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Trp-NH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-IL000329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-00100360.
                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Afargan MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-136888/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PEPT-) PEPTOR LID.
||:::|
2 YWVWWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9965508-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-DEC-1998;
                                                                                                                                                                                                    20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hornik V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                              AAY76792;
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Gaps

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0; Indels

3; Mismatches

3; Conservative

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic; somatotropin release inhibiting factor; somatostatin receptor subtype; synthesis; antiarterioselerotic; immunosuppressive; cytostatic; cancer; antialiameneleroy; somatostatin receptor ligand; atherosclerosis; autoimmune disease; diabetic-associated complication; endocrine disorder; inflammation; gastrointestinal disorder; restenosis;
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New backbone cyclized somatostatin analogs are e.g. useful in the treatment of atherosclerosis, autoimmune diseases and cancers.
                                                                      ö
                                                                0; Indels
      Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Backbone cyclised somatostatin analogue PTR 3177.
   Score 32; DB 3; I
Pred. No. 1.7e+06;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "D form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gellerman G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 12; Page 21; 30pp; English
                                                                                                                                                                                                                                                                                                                                                               ABP53416 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "amidated'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pancreatitis; post-surgical pain
84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-DEC-2000; 2000US-00734583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-00100360.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hornik V, Afargan MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AFAR/) AFARGAN M M.
(GELL/) GELLERMAN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-681319/73.
   Query Match
Best Local Similarity
                                                                                                                                                                     | | | : : : |
2 YWKVCW 7
                                                                                                                            YWXXXW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HORN/) HORNIK V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2002052315-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                           ABP53416;
                                                            Matches
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ABPS 3416

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the existence of metastases, it being labeled with a detectable probe. The present sequence represents a backbone cyclised somatostatin analogue from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method of identifying a ligand that can mediate the biological activity of target protein via inhibition of the binding of target protein to a binding partner ligand comprising screening first combinatorial library having first member ligands for binding to target protein to identify target-binding ligand(s). The method is useful for identifying ligands that can mediate the biological activity of target proteins via inhibition of the binding of target protein to a binding partner ligand. The invention does not require the natural binding partner ligand. The seagent. The need for the natural binding partner will the use of complementary combinatorial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identification of ligand that can mediate biological activity of target protein, comprises screening first combinatorial library having first member ligands for binding to target protein to identify target-binding
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    libraries. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                ligand identification; peptide library; complementary combinatorial library; tyrosine tRNA synthetase.
                                                                                   Score 32; DB 5; Lengtn /;
Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.2%; Score 32; DB 8; Length 7; 50.0%; Pred. No. 1.7e+06; ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Frelinger JA, Hyde-Deruyscher RP;
                                                                                                                                                                                                                                                                                                                                                                    Tyrosine tRNA synthetase binding peptide group 2 motif.
                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; SEQ ID NO 94; 98pp; English.
                                                                                                                                                                                                                                                                           ADJ25834 standard; peptide; 7 AA.
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                                                                                                 84.2%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kay BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KARO-) KARO BIO AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-068186/07.
                                                                                                 Query Match
Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                 YWKVCW
                                                                                                                                                              2 YWXXXW
                                                                    Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6617114-B1.
                                                                                                                                                                                                                                                                                                                                     20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-1997;
31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fowlkes DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-SEP-2003
                                                                                                                                                                                                                                                                                                        ADJ25834;
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2 YWXXXW

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PTP-D1; PTP-D2; PCR; polymerase chain reaction; amplify; subfamily; protein tyrosine phosphatase; PTP; catalytic domain; PTPase; antibody; glycoprotein; cancer; diabetes; cellular; human; phosphotyrosine metabolism.
                                                                                                                                                                                                                                                                                                                        (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                        PTP-D1/D2 primer #58 peptide
                                                                                                                                                                                                                                                                                                                                              Ullrich A, Moller N,
                                                                                                                                                                     Misc-difference
                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                            05-AUG-1993;
                    25-MAR-2003
26-AUG-1994
                                                                                                                                                                                                                                WO9403611-A2
                                                                                                                                                                                                                                                                                                  05-AUG-1992;
                                                                                                                                                                                                                                                     17-PEB-1994
                                                                                                                                      Synthetic
AAR46290;
vasculitis; pregnancy associated toxaemia; transplantation, surgery. Peptides which bind to endothelin receptors may act as agonists or antagonists depending on whether they effect or block the activity of the receptor. They may be used to modulate conditions such as cardiogenic shock, hypertension, pulmonary hypertension, acute myocardial infarction, uraemia, Crohn's disease and ulcerative colitis which are associated with increased levels of endothelin. Increased endothelin levels are also observed following orthotopic liver transplantation and major abdominal sepsis, congestive heart failure, coronary spasm, cyclosporine nephrotoxicity, vasculitis and pregnancy associated toxaemia. (See also AAR48782-R48933). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                      Endothelin; agonist; antagonist; peptide; receptor; cardiogenic shock; hypertension; pulmonary hypertension; acute mycozadial infarction; uraemia; Crohn's disease; ulcerative colitis; sepsis; nephrotoxicity; congestive heart failure; coronary spasm; cyclosporine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endothelin receptor binding compounds - for treating hypertension, cancer, psoriasis, atherosclerosis, hyperplasia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                  Geysen HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 28; DB 2; I Pred. No. 1.7e+06;
                                                                                                                                                 Peptide which binds endothelin receptors.
                                                                                                                                                                                                                                                                             /note= "D-form residue."
                                                                                                                                                                                                                                                                                                                                                                                                                  Simon RJ,
                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                   AAR48807 standard; peptide; 6 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Page 27; 40pp; English.
                                                                                                                                                                                                                                                                                                                                               93WO-US007166.
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                                                                                                                                                                                                                                                                                                                                                                      92US-00923703
                                                                                                                                                                                                                                                                                                                                                                                                                  Stauber GB,
                                                                                                                (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-065598/08.
                                                                                                                                                                                                                                                                                                                                                                                           (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
           9
||:::|
YWWPDW 6
                                                                                                                                                                                                                                                      Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                  Spellmeyer DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                               30-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                      30-JUL-1992;
                                                                                                               25-MAR-2003
12-AUG-1994
                                                                                                                                                                                                                                                                                                    WO9403483-A1
                                                                                                                                                                                                                                                                                                                          17-FEB-1994.
                                                                                                                                                                                                                                 Synthetic.
                                                                                        AAR48807;
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                                           RESULT 1(
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Bach-Moller K;

93WO-EP002086. 92US-00923740.

note= "Undefined amino acid" /note= "Undefined amino acid"

Location/Qualifiers

(first entry)

(revised)

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The sequences given in AAR46290-91 are peptides which were used to design the primers given in AAG57005-06 which were used in the amplification and identification of the PTPases, PTP-D1 and PTP-D2. PTP-D1 and PTP-D2 which have slightly different structures from previously reported PTPs. Members of the PTP-D subfamily are characterised by having one, two or three identified amino acid changes in previously defined consenaus sequences in the catalytic phosphatase domains of known PTPases. PTP-D, its antibodies or the DNA encoding PTP-D molecules may be used for activity of PTP-D protein or glycoprotein associated with a cell or tissue. This may be utilised in methods for identifying susceptibility to cancer, diabetes or other diseases associated with alterations in cellular phospho- tyrosine metabolism. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                        New protein tyrosine phosphatase(s), DNA encoding PTP-D and antibodies to PTP-D - for identifying normal or mutant PTP-D genes, treating or diagnosing e.g. cancer, diabetes or diseases associated with altered tyrosine phosphate metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 28; DB 2; Lengtn o, Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                              Example 1; Page 43; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW43021 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.7%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
WPI; 1994-065699/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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1 FWXMXW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 YWXXXW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW43021;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
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Gaps

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0; Indels

4; Mismatches

2; Conservative

Matches

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AAR46290 standard; protein; 6 AA.

RESULT 11 AAR46290 ID AAR4 XX

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Misc-difference 3
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FFFFX8X6X8X8X6XIX8XFFX8XCCCCCCCCCCCCX8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; protein tyrosine phosphatase; antibody; intracellular domain; LAR; CD45; PTP; diagnosis; insulin resistance related disease; syndrome X; non-insulin dependent diabetes mellitus; arteriosclerosis; therapy; heart disorder; signature motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This peptide corresponds to a conserved region of known protein tyrosine phosphatases (PTP). A sense primar (see AAV04937) based on this peptide was used in the PCR amplification of mouse neural tube cDNA. A 359 bp segment was isolated and used to screen a mouse brain cDNA library to identify several overlapping clones containing a 3.2 kb sequence (see AAV404936) encoding a novel PTP-NP (for neural and pancreatic) receptor (see AAW43023) that can be used for modulating growth, differentiation and survival of cells and for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein tyrosine phosphatase-neural and pancreatic poly:peptide(s) and related nucleic acid - useful for modulating growth, differentiation and
                                                                                          Protein tyrosine phosphatase-neural and pancreatic; PTP-NP; mouse; cell growth; cell differentiation; cell survival; drug screening; tissue injury; wound healing; pancreas; neural cell; transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 28; DB 2; Length 6;
Pred. No. 1.7e+06;
3; Mismatches 0; Indels
                                                       Protein tyrosine phosphatase conserved peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  related nucleic acid - useful for modulat:
survival of cells and for drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein tyrosine phosphatase motif #2.
                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 57; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY81787 standard; peptide; 6 AA
                                                                                                                                                                                                                                                         /label= Ile, Val
                                                                                                                                                                                                                                                                                                                                                                            97WO-US011519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.7%;
50.0%;
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                06-JUL-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M, Flanagan JG;
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FWRMXW
                                                                                                                                                                                                                                    Misc-difference
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                                                                                                                                                                          Synthetic
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Matches

RESULT 13

셤

Chiang

Location/Qualifiers

Unidentified

Key

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This sequence represents a motif of a protein tyrosine phosphatases. The invention relates to an antibody of the invention that has sites specifically recognising the intracellular domain of two or more protein tyrosine phosphatases (PTPs). The antibody is useful for the detection and assay of PTP including novel phosphatases generated by cloning; and diagnosis, treatment and prevention of insulin resistance related diseases and non-insulin dependent diabetes mellitus, syndrome X and arteriosclerosis and heart disorders
                                                                                                                                                                                                                                                                                                                  Antibody for diagnosis and treatment of insulin resistance disorders and syndrome X recognises the intracellular domains of tyrosine kinases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fibronectin; collagen-binding proteins; inhibit cell adhesion; regulate cell matrix interactions; tumourigenesis; metastasis; wound repair; homostasis; thrombospondin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 28; DB 3; Length 6;
Pred. No. 1.7e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
'label= Arg, Glu, Leu
                                 /label= Val, Ile, Cys
                                                                                                                                                                                                                                              Tsujikawa K, Uchino Y;
                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 32; 83pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR62543 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.7%;
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                                                                                                                                       99WO-JP003656.
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                                                                                                                                                                                                             (FUSO ) FUSO PHARM IND LTD
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                                                                                                                                                                                                                                                                               WPI; 2000-182215/16.
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Best Local Similarity
Matches 4; Conserv
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FWXMXW
                Misc-difference
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                                                                   WO200002922-A1
                                                                                                                                       06-JUL-1999;
                                                                                                                                                                          10-JUL-1998;
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16-DEC-1994
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                                                                                                      20-JAN-2000
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Peptides which bind to fibronectin and collagen-binding proteins - are used to inhibit fibronectin dependent cell adhesion to collagen matrices.
                                                                                                                                                                                                                                     Disclosure; Page 40; 51pp; English
WPI; 1994-183422/22
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Thrombospondin is a multi-functional protein capable of interacting with numerous molecules, eg. fibronectin. Peptides have been designed that are derived from the second type I repeat of human modothelial cell thrombospondin. The peptides can be used to bind to fibronectin or other related collagen-binding proteins to inhibit fibronectin-dependent cell adhesion to collagen matrices. The peptides interact directly with the gelatin-binding domain of fibronectin and inhibits the fibronectin function. (Updated on 25-MAR-2003 to correct PN field.)

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Sequence 7 AA;
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Length 7;
                   1; Indels
Score 28; DB 2; | Pred. No. 1.7e+06;
                  3; Mismatches
73.7%;
         Local Similarity 42.3
nes 3; Conservative
                                      GYWXXXW
                                                 1 GGWSKSW
 Query Match
                   Matches
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completed: January 3, 2005, 17:14:31

Job time : 149 secs

Search

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Gaps ; 0

AAY14751 standard; peptide; 7 AA. (first entry) 11-0CT-1999 AAY14751; AAY14751
AAY

Tyrosine phosphatase conserved domain.

Genetic proximity, gene expression, cell characterisation, homeobox gene; genetic defect, reverse transcriptase polymerase chain reaction, RT-PCR, kinase gene; protein phosphatase; P450; steroid receptor; cadherin.

# Homo sapiens

98WO-IL000625 97IL-00122793. 98IL-00126627. WO9934016-A2 28-DEC-1998; 29-DEC-1997; 16-OCT-1998; 08-JUL-1999.

WPI; 1999-419113/35. N-PSDB; AAZ18217. Vider B;

(GENE-) GENENA LTD

Example; Page 48; 102pp; English.

Identifying and characterizing cells by comparing the pattern of gene expression in a selected gene family.

The invention provides a new method for identifying and characterising cells. The method for determining the genetic proximity of a first cell and a second cell comprises: (a) obtaining the first cell and the second cell; (b) determining in the first cell and the second cell; (b) determining in the first cell and the second cell the pattern of expression of genes in a selected gene family; and (c) calculating a poximity index using a specified formula. The methods can be used for characterising cells, e.g. for determining the origin of a cell, its genetic status, whether it carries a genetic defect, or whether it is

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an individual, e.g. a fetus. They can also be used for determining the effect of a selected treatment on a test cell. They can also be used for determining the effect of a selected treatment on a test cell. They can also be used for obtaining cells capable of expressing an homeobox related desired property. The method uses reverse transcriptase polymerase chain reaction (RT-PCR) for determining the pattern of gene expression in a selected gene family. Sequences AAZI7803-Z18342 represent primers that can be used in the RT-PCR reactions to determine the pattern of gene expression. The gene family can be selected from a set of homeobox genes, kinase genes, protein phosphatase genes, P450 enzyme genes, steroid receptor superfamily genes or cadherin superfamily genes. Sequences AAY14603-813 represent conserved peptide motifs based on which the primers of the invention were designed
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 1.7e+06;
4; Mismatches 0; Indels
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33.3%;
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Best Local Similarity
Matches 2; Conserv
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TYPE: amino acid
STRANDEDNESS: eingle
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 737-3528
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SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 94, Appl Sequence 16, Appl Sequence 12, Appl Sequence 11, Appl Sequence 14, Appl Sequence 14, Appl Sequence 2, Appl Sequence 2, Appl Sequence 30, Appl Sequence 5, Appl Sequence 5, Appl Sequence 5, Appl Sequence 5, Appl Sequence 67, Appl Sequence 57, Appl Sequence 67, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 18, Appl 
                                                                                                                                        ; Search time 37 Seconds (without alignments)
12.547 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/iaa/SB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/GA_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-443-640-16
US-08-4446-345-12
US-08-951-260A-12
US-08-984-569A-11
US-09-9384-569A-14
US-09-143-697-2
US-09-743-697-2
US-09-743-697-2
US-09-743-697-2
US-08-52-971-5
US-08-65-971-5
US-08-991-258A-5
US-08-991-258A-6
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US-08-991-258-988-0
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
                    Copyright
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Maximum#DB#seq#Nength:#7.4
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88, Appl 88, Appl 98, Appl 15, Appl 16, Appl 17, Appl 2007, Ap 2007, Ap 21, Appl 18, Appl 5185431 5217869 5217869 5217869 191, Appl 191, Appl									
Sequence No. Patent No. Sequence Sequen			IG LIBRARIES			30			
US-08-477-134-88 US-08-477-489A-88 US-09-181-083-15 US-09-181-083-15 US-09-181-083-15 US-09-209-676-14 US-09-53-852-2007 US-09-53-852-2007 US-09-750-754-15 US-09-750-754-15 US-09-750-754-15 US-09-750-754-15 US-09-14 5217869-14 5217869-14 US-08-439-11-57-17 US-08-439-817-191	ALIGNMENTS	4	o OF DRUGS USIN COMBINATORIAL	/8 : AND NEIMARK, P.L.L.C. Street N.W., Suite 300	·	compatible PC-DOS/MS-DOS 1 Release #1.0, Version #1.3 R: US/09/069,827A	,359	PCT/US97/19638 11997 US 08/740,671 11996	28,005 ER: FOWLKES=4C ION:
2 US-08-477- 3 US-08-473- 3 US-08-181- 3 US-09-181- 3 US-09-181- 4 US-09-209- 4 US-09-209- 4 US-09-535- 4 US-09-750- 5 ST7-US94-0 6 S217869-18 6 S217869-18 1 US-08-439- 1 US-08-439-	Ā	9 .	FRELINGEK, JETTREY A HYDE-DERUYSCHER, RObin I VENTION: IDENTIFICATION COMPLEMENTARY	178 SS: DY AND NE th Street	A. FORM: Floppy disk	COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/WS-D SOPTWARE: PatentIn Release #1 NT APPLICATION DATA: APPLICATION NUMBER: US/09/069	FILING DATE: 30-Apr-1998 CLASSIFICATION: «Unknown» APPLICATION DATA: APPLICATION WUMBER: US 09 FILING DATE: 31-MAR-1998	APPLICATION NUMBER: PCT/ FILING DATE: 31-OCT-1997 APPLICATION NUMBER: US 0 FILING DATE: 31-OCT-1996 NEY/AGENT INFORMATION:	_ m_E : u
<b>ստաստաստաստաստաստաս</b>		cation US/C ION: FOWLKES, De	FRELINGER, HYDE-DERUY INVENTION: I	NUMBER OF SEQUENCES: 17 CORRESPONDENCE ADDRESS: ADDRESSEE: BROWDY STREET: 624 Ninth CITY: Washington	STATE: D.C. COUNTRY: U.S.A. ZIP: 20001 COMPUTER READABLE FORM: MEDIUM TYPE: Flopp	COMPUTER: IBM PC com OPERATING SYSTEM: PC SOFTWARE: Patentin R CURRENT APPLICATION DATA: APPLICATION NUMBER:	ILING DATE: 30-AP. LASSIFICATION: <u 31-ma<="" application="" data:="" date:="" iling="" number="" pplication="" td=""><td>APPLICATION NUMBER: FILING DATE: 31-OCT- APPLICATION NUMBER: FILING DATE: 31-OCT- NEY/AGENT INFORMATIC</td><td>NAME: COOPER, IVER P REGISTRATION NUMBER: REFERENCE/DOCKET NUM OMMUNICATION INFORMA TELEPHONE: (202) 628</td></u>	APPLICATION NUMBER: FILING DATE: 31-OCT- APPLICATION NUMBER: FILING DATE: 31-OCT- NEY/AGENT INFORMATIC	NAME: COOPER, IVER P REGISTRATION NUMBER: REFERENCE/DOCKET NUM OMMUNICATION INFORMA TELEPHONE: (202) 628
		7A-94 4, Applicat 6617114 INFORMATION LICANT: FOW	OF INV	R OF SE SPONDEN ADDRESSI STREET: CITY: W	STATE: D.C. COUNTRY: U.S ZIP: 20001 TER READABLE MEDIUM TYPE:	COMPUTER: OPERATING SOFTWARE: NT APPLICA	TLING TASSIF APPLICA PPLICA	APPLICATION PELLING DATE: APPLICATION PELLING DATE: FILING DATE: ATTORNEY/AGENT IN	AME: COEFERENCE MMUNICA
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Sequence 16, Application US/08443640

Patent No. 569140

GENERAL INFORMATION:
APPLICANT: NOREN, CHRISTOPHER J.
APPLICANT: EVANS, PAUL D.
TITLE OF INVENTION: BIDIRECTIONAL IN VITRO TRANSCRIPTION
TITLE OF INVENTION: DIRECTIONS
TITLE OF INVENTION: DIRECTIONS
TITLE OF SEQUENCES: 36

NORBER OF SEQUENCES: 36
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0
                                       Score 32; DB 4; Length 7; Pred. No. 3.8e+05; 3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 01915
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,640
FILING DATE: 18-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOVEL PROTEIN PHOSPHOTYROSINE PHOSPHATASES PTP-D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 29; DB 1;
Pred. No. 3.8e+05;
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ADDRESSEE: NEW ENGLAND BIOLABS, INC
STREET: 32 TOZER ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEPHONE: (508) 927-5054
TELEPHONE: (508) 927-1705
INFORMATION POR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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Sequence 12, Application US/08446345
Sequence 12, Application US/08446345
Sequence 12, Application US/08446345
Sequence 12, Application US/08446345
Sequence 12, Application Axel
APPLICANT: Woller, Niels P.H.
TITLE OF INVENTION: PHOSPHATASES PT
TITLE OF INVENTION: PHOSPHATASES PT
                                         84.2%;
50.0%;
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Best Local Similarity 42.9%;
Matches 3; Conservative
                                     Query Match
Best Local Similarity 50.0
Matches 3; Conservative
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STRANDEDNESS: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-443-640-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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                                                                                                                            2 YWXXXW 7
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1 YWWPDW 6
US-09-069-827A-94
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Aoki, Nachito

APPLICANT: Aoki, Nachito

APLICANT: Aoki, Nachito

TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20

TITLE OF INVENTION: AND RELATED PRODUCTS AND METHODS

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: Suite 4700

STREET: Suite 4700
                                                              STREET: INDEAD AVEILLE OF THE AMMETICASE STATE:

COUNTRY: U.S.A.

ZIP: 10036-271

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ATTORNEY/AGENT INFORMATION:
NAME: COLUZI, LAURA A.
REGISTRATION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 7683-054
TELEPHAN: (212) 790-9990
TELEFRAN: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTESD for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,260A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: US/08/951,260A
October 16, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-951-260A-2; Sequence 2, Application US/08951260A; Patent No. 6004791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 YWXXXW 7
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1 FWXMXW 6
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Sequence 14, Application US/08884569A
Falent No. 6399326
GENERAL INFORMATION:
APPLICANT: CHIANG, MING-KO
TITLE OF INVENTION: RECEPTOR TYROSINE PHOSPHATASE, AND USES RELATED THERETO
FILE REPERENCE: HWV-020.01
CURRENT APPLICATION NUMBER: 60/021,040
FRICH FILING DATE: 1996-07-02
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 15
LENGTH: 6
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              Description of Artificial Sequence: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09430626A
Patent No. 648260S
GENERAL INPORMATION:
APPLICANT: Aoki, Naohito
Allrich, Axel
TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND RELATED PRODUCTS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6;
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Pred. No. 3.8e+05;
2; Mismatches (
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APPLICATION NUMBER: US/09/430,626A
FILING DATE: 29-0ct-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/951,260
FILING DATE: October 16, 1997
APPLICATION NUMBER: 60/030,860
FILING DATE: No. 6442605ember 13, 199
APPLICATION NUMBER: 60/1897/00946
FILING DATE: June 17, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
OTHER INFORMATION: Description of OTHER INFORMATION: peptide NAME/KEY: MOD_RES COCATION: (3)
OTHER INFORMATION: Arg or Gln NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.78;
66.78;
                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (5) OTHER INFORMATION: Ile or Val
US-08-884-569A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 73.7
Best Local Similarity 66.7
Matches 4; Conservative
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1 FWXMXW 6
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GENERAL INFORMATION:
APPLICANT: CHIANG, MING-KO
APPLICANT: FLANAGAN, JOHN G.
TITLE CANT: FLANAGAN, JOHN G.
TITLE OF INVENTION: RECEPTOR TYROSINE PHOSPHATASE, AND USES RELATED THERETO
FILE REFERENCE: HMV-020 01
CURRENT APPLICATION NUMBER: US/08/884,569A
CURRENT PILING DATE: 1997-06-27
PRIOR APPLICATION NUMBER: 60/021,040
PRIOR FILING DATE: 1996-07-02
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28; DB 3; Length 6; Pred. No. 3.8e+05; 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Xaa" in positions 3 and 5 stand
for an unspecified amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.7%; Score 28; DB 3; Le
50.0%; Pred. No. 3.8e+05;
tive 3; Mismatches 0;
                           PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 60/030,860

FILING DATE: NO. 6004791ember 13, 199

APPLICATION NUMBER: PCT/1897/00946

FILING DATE: JUNERATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 227/004

TELECOWMUNICATION:

TELEPHONE: (213) 955-0440

TELEPHONE: (213) 955-0440

TELEPAX: 67-3510

SEQUENCE CHARACTER.STICS:

LENGTH: 6 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08884569A Patent No. 6399326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Ile or Val
US-08-884-569A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 65...
A. Conservative
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Best Local Similarity 50.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
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FWRMXW 6
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1 FWXMXW 6
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RESULT 6 US-08-884-569A-14

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: MOLLER, KARIN B.
APPLICANT: MOLLER, KARIN B.
TITLE OF INVENTION:
FULL REPRENDICT:
OURRENT APPLICATION NUMBER: US/09/361,096A
CURRENT APPLICATION NUMBER: US/09/361,096A
FRIOR PRILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 08/49,609
PRIOR PELING DATE: 1995-03-24
PRIOR APPLICATION NUMBER: 08/036,210
PRIOR APPLICATION NUMBER: 08/036,210
PRIOR SEQ ID NOS: 53
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATENTIN UVE: 2.1
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                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: "Xaa" in positions 3 and 5 stand for an unspecified amino acid. SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Consensus OTHER INFORMATION: sequence NAME/KEY: MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 73.7%; Score 28; DB 4; Length 6; Best Local Similarity 66.7%; Pred. No. 3.8e+05; Matches 4; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 227/004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Variable amino acid US-09-361-096A-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 46, Application US/09361096A
Patent No. 6492495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
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Best Local Similarity
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1 FWXMXW 6
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1 FWXMXW 6
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US-09-361-096A-46
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SEQ ID NO 46
LENGTH: 6
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RESULT 9 US-09-743-492A-5

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Sequence 5, Application US/09743492A

Patent No. 6709843

GENERAL INFORMATION:
APPLICANT: YAMAMOTO, Hiroshi
TAPLICANT: TSUJIKAWA, Kazutake
APPLICANT: TSUJIKAWA, Kazutake
TITLE OF INVENTION: AVTIBODIES SPECIFIC FOR INTRACELLULAR DOMAIN OF PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
FILE REFERENCE: 19036/37023
CURRENT APPLICATION NUMBER: US/09/743,492A
CURRENT FILING DATE: 1998-07-10
FRIOR FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial sequence
FEMTURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Unknown Organism: Consensus Amino OTHER INFORMATION: Acid Sequence in Cytoplasmic Domain of Known PTPB. Patent No. 67109843
FEATURE: NAME/KEY: SITE
LOCATION: (3)
OTHER INFORMATION: Xaa= Arg, Glu or Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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APPLICANT: Aboki, Nachito
Ullrich, Axel
TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
AND RELATED PRODUCTS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28; DB 4; Length 6;
Pred. No. 3.8e+05;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/430,626A
FILING DATE: 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSED for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/243,687
FILING DATE: 16-Sep-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (5)
; OTHER INFORMATION: Xaa= Val, Ile or Cys
US-09-743-492A-5
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ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Sulte 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10243687; Settent No. 6797501; Patent No. 6797501; GENERAL INFORMATION:
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66.7%;
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Best Local Similarity 66.7
Matches 4; Conservative
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1 FWXMXW 6
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; MOLECULE TYPE: peptide US-07-973-235A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                   1 GYWXXXW 7
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1 GGWSKSW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 YWXXXW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : |::||
2 FWRMXW
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                                                                                                                                                                                                                                                           RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: "Xaa" in positions 3 and 5 stand for an unspecified amino acid. SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30, Application US/07973235A
Fatent No. 5491130
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lowe, Price, LeBlanc & Becker
STREET: Suite 300, 99 Canal Center Plaza
CITY: Alexandria
STATE: Viscandria
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 28; DB 4; Length 6;
Pred. No. 3.8e+05;
2; Mismatches 0; Indels
               FILING DATE: October 16, 1997
APPLICATION NUMBER: 60/030,860
FILING DATE: NO. 679750lember 13,
FILING DATE: MUMBER: PCT/1897/0094,
FILING DATE: June 17, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                          NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 227/004
TELECOMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
CEMPATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/973,235A
FILING DATE: 19921110
CEMPASIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: ROBERT L. Price
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                         INFORMATION FOR SBQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.7%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
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Best Local Similarity 66.7
Matches 4; Conservative
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1 FWXMXW 6
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OTHER INFORMATION: /note= "Let 'X' located at position
OTHER INFORMATION: 1 represent either Histidine or Aspartic Acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
ITILB OF INVENTION: PHOSPHATASE, PTP LAMBDA
ITILB OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
ITILB OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
ITILB OF INVENTIONE
ITILB OF IN
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OTHER INFORMATION: /note= "Let 'X' located at position
OTHER INFORMATION: 6 represent either Isoleucine or Valine."
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                                                                                           1; Indels
    Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CARRENT APPLICATION DATA:
FILING DATE:
Score 28; DB 1; I
Pred. No. 3.8e+05;
3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger R.
REGISTRATION NUMBER: 33 055
REFERENCE/DOCKET NUMBER: P1033
TELEPHONE: (415) 225-3216
TELEPHONE: (415) 952-9881
TELEPAX: 910 371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-652-971-5; Sequence 5, Application US/08652971; Patent No. 5814507
73.78;
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Best Local Similarity 50.0
Matches 3, Conservative
Query Match
Best Local Similarity 42.9
Matches 3; Conservative
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MOLECULE TYPE: protein
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LOCATION: 1..2
OTHER INFORMATION: /note= "Let 'X' located at position
OTHER INFORMATION: 1 represent either Histidine or Aspartic Acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 6..7

CTHER INFORMATION: 6 represent either Isoleucine or Valine. US-08-991-258A-5
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APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.7%; Score 28; DB 2; Length 7; 50.0%; Pred. No. 3.8e+05; ive 3; Mismatches 0; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,258A
FILING DATE: 17-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,971
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/POCKET NUMBER: A-63478-3/WHD/WTK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 460 Point San Bruno Blvd.
CITY: South San Francisco
STATE: California
COUNTR: United States
ZIP: 94080
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08769399
Patent No. 5976852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 50.0
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MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 YWXXXW 7
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2 FWRMXW 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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| Sequence 5, Application US/08991258A
| Patent No. 59288A-5
| APPLICANT: Cheng, Jill
| APPLICANT: Cheng, Laurenche Novel Kappa/MU-LIKE PROTEIN TYROSINE
| TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
| NUMBER OF SEQUENCES: 10
| CORRESPONDENCE ADDRESS: ADDRESSE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP
| STREET: 4 Embarcadero Center, Suite 3400
| CITY: San Francisco
| STARET: California | STARET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                           APPLICANT: KOUSLIS, DAILS D.
APPLICANT: Sipes, John M.
APPLICANT: Sipes, John M.
APPLICANT: Guo, Neng-hua
APPLICANT: Guo, Neng-hua
APPLICANT: Guo, Neng-hua
APPLICANT: Negre, Eric
TITLE OF INVENTION: Peptide Inhibitors of Pibronectin and
TITLE OF INVENTION: Related Collagen-Binding Proteins
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITRE: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USAN
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTON DATA:
APPLICATION NUMBER: US/08/462,720
FILING DATE: 05-UN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DOW, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 015280-023110US
TELEPHONE: (415) 326-2400
TELEFRAX: (415) 326-2400
TELEFRAX: (415) 326-2402
TELEFRAX: (415) 326-2422
INFORMATION FOR SEC ID NO: SEQUENCE CHARACTERISTICS:
TENENALLION CARRESTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.7%; Score 28; DB 2; I
42.9%; Pred. No. 3.8e+05;
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                                                                                                                  Sequence 30, Application US/08462720 Patent No. 5849701 GENERAL INFORMATION: GENERAL REDEATE, David D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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Best Local Similarity
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                                                                                 US-08-462-720-30
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Gaps

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ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Ginger R.

REGISTRATION NUMBER: 33,055

REFERENCE/DOCKET NUMBER: P1033

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 952-9881

TELEX: 910 371-7168

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: 11near

MOLECULE TYPE: protein

FRATURE:

NAME/KEY: Active-site

LOCATION: 1.2

LOCATION: 1.2

OTHER INFORMATION: / note= "Let 'X' located at position

OTHER INFORMATION: / note= "Let 'X' located at position

OTHER INFORMATION: / note= "Let 'X' located at position

OTHER INFORMATION: / note= "Let 'X' located at position

OTHER INFORMATION: / note= "Let 'X' located at position

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OTHER INFORMATION: / note= "Let 'X' located at position

OTHER INFORMATION: / note= "Let 'X' located at position

OTHER INFORMATION: / note= "Let 'X' located at position

OTHER INFORMATION: 6 represent either Isoleucine or Valine."

US-08-769-399-5
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Search completed: January 3, 2005, 17:27:14 Job time : 37 sece

2 YWXXXW 7 :|::|| 2 FWRMXW 7

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0; Gaps

Query Match 73.7%; Score 28; DB 2; Length 7; Best Local Similarity 50.0%; Pred. No. 3.8e+05; Matches 3; Conservative 3; Mismatches 0; Indels

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100.0%; Score 38; DB 13;
100.0%; Pred. No. 1.5e+06;
ive 0; Mismatches 0;
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US-10-418-943-48
; Sequence 48, Application US/10418943
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Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYWXXXW 7
                                              TYPE: PRT
ORGANISM: peptide
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Sequence 46, Appli
Sequence 46, Appli
Sequence 10, Appl
Sequence 38, Appl
Sequence 183, Appl
Sequence 195, App
Sequence 65, Appl
Sequence 76, Appl
Sequence 76, Appl
Sequence 76, Appl
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Sequence 48, App
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                                                                                                                                (without alignments)
18.116 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUDLISHER APPLICATIONS ANA TOTAL STATE AND SALES AND SAL
                                                                                                               January 3, 2005, 17:15:18 ; Search time 139 Seconds
               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-418-943-48
US-10-818-93-1
US-10-314-232-46
US-10-858-271-10
US-09-84-767A-38
US-09-63-252-53
US-10-052-578-195
US-10-052-578-195
US-10-190-082-76
US-10-190-082-76
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                                                                                                                                                                                                                                                                                               1599051 segs, 359727711 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published_Applications_AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Listing first 45 summaries
                                                                                - protein search, using sw model
                                                                                                                                                                                                                                              BLOSUM62DX | Gapext 0.5
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and is derived by analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                              US-10-046-922-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length
                                                                                                                                                                                                               1 GYWXXXW 7
                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum_DB_seq_length: 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                 Perfect score:
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8
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Sequence 198, App
Sequence 76, Appl
Sequence 8, Appl
Sequence 53, Appl
Sequence 496, App
Sequence 196, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 1886, Appl
Sequence 1886, Appl
Sequence 1586, Appl
Sequence 1586, Appl
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Sequence 525, App
Sequence 84, Appl
Sequence 69, Appl
Sequence 101, Appl
Sequence 25, App
Sequence 207, App
Sequence 19, Appl
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Sequence
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Sequence
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Sequence 67, Application US/10046922

Publication No. US20020164667A1

GENERAL INFORMATION:

APPLICANT: Alitalo, Kari

APPLICANT: Koivunen, Erkki

APPLICANT: Koivunen, Erkki

APPLICANT: Kubo, Hajime

TITLE OP INVENTION: VEGFFA

CURRENT APPLICATION NUMBER: US/10/046,922

CURRENT APPLICATION NUMBER: US/10/046,922

CURRENT PILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin version 3.0

SEQ ID NO 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: SITE LOCATION: (4)..(6)
OTHER INFORMATION: X at position 4-6 is any amino acid
US-10-053-520-195
US-10-053-498B-183
US-10-053-498B-183
US-10-053-498B-195
US-10-258-146A-41
US-10-258-146A-53
US-10-328-953-198
US-10-328-953-198
US-10-258-144-88
US-10-258-144-88
US-10-258-144-88
US-10-435-953-198
US-10-435-953-198
US-10-435-953-198
US-10-436-953-198
US-10-436-953-198
US-10-436-951-188
US-10-436-949-525
US-10-436-949-525
US-10-436-949-525
US-10-436-949-525
US-10-374-466-14
US-10-374-466-14
US-10-374-466-14
US-10-374-455-9555
US-10-374-466-14
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. Gaps

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Length 7; Indels

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OTHER INFORMATION: "Xaa" in positions 3 and 5 stands for an unspecified amino acid. SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/10243687
Publication No. US20030073120A1
GENERAL INFORMATION: Aoki, Naohito
TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
AND RELATED PRODUCTS AND METHODS
APPLICATION NUMBER: U.S. 60/030,964
FILING DATE: No. US20020169303Alember 15, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFREENCE/DOCKET NUMBER: 225/298
TELECOMUNICATION INFORMATION:
TELEPONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPAGIBLE
COMPUTER: IBM COMPAGIBLE
CORREATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/243,687
FILING DATE: 16-58p-2002
CLASSIFICATION NUMBER: US/09/430,626A
FILING DATE: 29-0ct-1999
APPLICATION NUMBER: 08/951,260
FILING DATE: October 16, 1997
APPLICATION NUMBER: 60/030,860
FILING DATE: NO. US2003073120Alember 13, 1996
APPLICATION NUMBER: PCT/1897/00946
FILING DATE: UNDER: PCT/1897/00946
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.7%; Score 28; DB 13; Length 6; 66.7%; Pred. No. 1.5e+06;
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STATE: California
COUNTRY: U.S.A.
ZIP: 9071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 227/004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      storage
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Best Local Similarity
Matches 4; Conserv
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1 FWXMXW 6
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US-10-243-687-2
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US-10-087-993-1
| Sequence 1, Application US/10087993
| Publication No. US20020169303A1
| GENERAL INFORMATION:
| APPLICANT: Ullrich, Axel
| Acki, Nacohitco |
| Kim, Yeeng Woong |
| Wang, Hong Yang |
| Chen, Zhengjun |
| Naylor, Oliver |
| Kharitonenkov, Alexei Igorevich |
| Kharitonenkov, Alexei Igorevich |
| TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDP1, CLK, |
| AND SIRP POLYPEPTIDES AND RELATED |
| Chen, Chengjun |
| Chen, Chengjun |
| Chen, Chengjun |
| Chen, Zhengjun |
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COMPUTER: IBM COMPAGINE
COPERATING SYSTEM: IBM P.C. DOS 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/087,993
FILING DATE: 05-Mar-2002
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US/08/877,150
APPLICATION NUMBER: US. 60/019,629
FILING DATE: June 17, 1997
APPLICATION NUMBER: US. 60/023,485
FILING DATE: August 9, 1996
APPLICATION NUMBER: US. 60/033,485
FILING DATE: NOW USER: US. 60/033,486
FILING DATE: DECEMBER: US. 60/033,486
FILING DATE: DECEMBER: US. 60/033,486
                                          GENERAL INFORMATION:
APPLICANT: Segall, Anca
APPLICANT: Segall, Anca
APPLICANT: Segall, Anca
TITLE OF INVENTION: RECOMBINATION MODULATORS AND METHODS;
TITLE OF INVENTION: FOR PRODUCING AND USING THE SAME;
FILE REFERENCE: 011443 008-959
CURRENT APPLICATION NUMBER: 08/10/418,943
CURRENT FILNG DATE: 2003-04-17;
PRIOR APPLICATION NUMBER: 09/602,087
PRIOR APPLICATION NUMBER: 09/602,087
RICHERING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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Pred. No. 1.5e+06;
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ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             storage
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                     Publication No. US20040002441A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Homo sapiens
US-10-418-943-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||:::|
1 YWCYWW 6
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                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: "Xaa" in positions 3 and 5 stand for an unspecified amino acid.
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Consensus OTHER INFORMATION: sequence
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Pred. No. 1.5e+06;
2; Mismatches 0; Indels
                                                                                                                                                                                                                  Score 28; DB 14; Length 6; Pred. No. 1.5e+06; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MOD RES
LOCATION: (3)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (5) 
; OTHER INFORMATION: Variable amino acid
US-10-314-232-46
             TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELECOMMUNICATION INFORMATION:
                                  TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.7%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
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Best Local Similarity
Matches 4; Conserv
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1 FWXMXW 6
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FWXMXW 6
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                                                                                                                                                                                          US-10-243-687-2
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RESULT

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Sequence 10, Application US/10858271

Sequence 10, Application US/10858271

Sequence 10, Application No. US2004025982841

GENERAL INFORMATION:

APPLICANT: Devicer. Philip M.

APPLICANT: Potter. Philip M.

APPLICANT: Houghton, Peter J.

TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of TITLE OF INVENTION: COMPARE: 2040-66-01

FILE REPERENCE: 2004-06-01

PRIOR APPLICATION NUMBER: US/09/595,682

PRIOR PILING DATE: 1998-02-19

PRIOR PILING DATE: 1998-02-19

PRIOR APPLICATION NUMBER: PCT/US99/03171

PRIOR APPLICATION NUMBER: PCT/US99/03171

PRIOR APPLICATION NUMBER: PCT/US99/03171

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patent IN Ver. 2.0

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APPLICANT: Ley, Arthur C.
APPLICANT: Luneau, Christopher J.
APPLICANT: Luneau, Christopher J.
APPLICANT: Ladder, Robert C.
TITLE OF INVENTION: NOVEL ENTERCKINASE CLEAVAGE SEQUENCES;
FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT
CURRENT APPLICATION NUMBER: US 09/597,321
CURRENT APPLICATION NUMBER: US 09/597,321
FRIOR FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin Version 3.1
SEQ ID NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: synthetic enterokinase cleavage sequence US-09-884-767A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 7;
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Pred. No. 1.5e+06;
4; Mismatches 0
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APPLICANT: DYAX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-563-222-53
; Sequence 53, Application US/09563222
; Publication No. US20030079253A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Oryctolagus cuniculus
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ORGANISM: Artificial Sequence
PEATURE:
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Best Local Similarity 33.3
Matches 2; Conservative
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Best Local Similarity 50.0
Matches 3; Conservative
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US-10-190-082-76
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CURRENT APPLICATION NUMBER: 08/961,707
PRIOR PILING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 321
SOFTWARE: WordPerfect 8.0 for Windows
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      APPLICANT: Hiatt, Andrew
APPLICANT: Hein, Mich B.
TITLE OF INVENTION: INMUNOCLOBULIN BINDING PROTEIN ARRAYS IN
TITLE OF INVENTION: EUKARYOTIC CELLS
FILE REPERENCE: 310098.406
CURRENT APPLICATION NUMBER: US/09/563,222
CURRENT APPLICATION NUMBER: 2000-05-02
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 53
LENGTH: 7
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Publication No. US20030134787A1
GENERAL INFORMATION:
APPLICANT: Sloan-Kettering Institute for Cancer Research
APPLICANT: Rothman, James E.
APPLICANT: Mayhew, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: peptide in m13 coliphage US-10-052-578-183
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50.0%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 33...
2, Conservative
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Best Local Similarity 50.0
Matches 3; Conservative
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Houghton, Alan
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CRGANISM: Mus musculus
US-09-563-222-53
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2 HWWDWW 7
GENERAL INFORMATION:
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US-10-052-578-195
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US-10-052-578-183
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APPLICANT:
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APPLICANT: Hartl, Ulrich
APPLICANT: Ouerfelli, Ouathek
APPLICANT: Moroi, Yoichi
TILE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
FILE REFERENCE: 11746/46003
CURRENT PEPLICATION NUMBER: US/10/052,578
CURRENT PILING DATE: 2002-01-17
PRIOR REPLICATION NUMBER: 08/961,707
PRIOR FILING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 321
SOFTWARE: WordPerfect 8.0 for Windows
LENGTH: 7
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US-10-082-65

Sequence 65, Application US/10190082

Publication No. US20030148264A1

GENERAL INFORMATION:
APPLICANT: Lasky, Lawrence A.
APPLICANT: Sidhu, Sachdev S.
TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS
FILE REPERENCE: P1905R1

CURRENT APPLICATION NUMBER: US/10/190,082

CURRENT FILING DATE: 2002-07-03

PRIOR APPLICATION NUMBER: US 60/303,634

PRIOR PLIANG DATE: 2001-07-06

NUMBER OF EQ ID NOS: 683

SEQ ID NO 65

LENGTH: APPLICATION NUMBER: US 60/303,634

PRIOR PLIANG DATE: 2001-07-06

NUMBER OF SEQ ID NOS: 683

LENGTH: APPLICATION NUMBER: US 60/303,634
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APPLICANT: Lasky, Lawrence A.
APPLICANT: Sidhu, Sachev S.
APPLICANT: Held, Helke A.
TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS
FILE REFERENCE: P1905R1
CURRENT APPLICATION NUMBER: US/10/190,082
CURRENT FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US 60/303,634
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Pred. No. 1.5e+06;
4; Mismatches 0
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Publication No. US20030148264A1
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ORGANISM: Artificial Sequence
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Best Local Similarity 33.3%;
Matches 2; Conservative
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Best Local Similarity 33.3%;
Matches 2; Conservative
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2 HWQMLW 7
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CURRENT FILING DATE:
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; Sequence 183, Application US/10053520
; Publication No. US20030166530A1
; GENERAL INFORMATION:
   APPLICANT: Sloan-Kettering Institute for Cancer Research
   APPLICANT: Rothman, James E.
   APPLICANT: How, Mark
   APPLICANT: How, Mark
   APPLICANT: Howelven, Alan
   APPLICANT: Howefaell, Ulrich
   APPLICANT: Horefaell, Ouathek
   APPLICANT: Ourich
   APPLICANT: Woroi, Yoich
   TILLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
   FILE REFERENCE: 11746/46004
   CURRENT APPLICATION NUMBER: US/10/053,520
   CURRENT FILING DATE: 2002-10-01
   PRIOR APPLICATION NUMBER: 08/961,707
   PRIOR APPLICATION NUMBER: 08/961,707
   NUMBER OF SEQ ID NOS: 321
   SOFTWARE: WordPerfect 8.0 for Windows
   FERSION OF 183
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APPLICANT: Houghton, Alan
APPLICANT: Houghton, Alan
APPLICANT: Hardin, Ulrich
APPLICANT: Ouerfelli, Ouethek
APPLICANT: Moroi, Yoichi
TILE OF INVENTION: CONVIGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
FILE REFERENCE: 11746/46004
CURRENT APPLICATION NUMBER: US/10/053,520
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Pred. No. 1.5e+06;
4; Mismatches 0; Indels
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Publication No. US20030166530A1
GENERAL INFORMATION:
APPLICANT: Sloan-Kettering Institute for Cancer Research APPLICANT: Rothman, James E.
APPLICANT: Mayhew, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ), OTHER INFORMATION: peptide in m13 coliphage US-10-053-520-183
                                                                                TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                               71.18;
33.38;
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PRIOR FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 683
SEQ ID NO 76
LENGTH: 7
                                                                                                                                   OTHER INFORMATION: Synthetic US-10-190-082-76
                                                                                                                                                                                           Query Match
Best Local Similarity 33.3.
Thea 2; Conservative
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1 HWIETW 6
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2 HWWDWW 7
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US-10-053-520-183
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APPLICANT: Hoe, Mee H.
APPLICANT: Houghton, Alan
APPLICANT: Houghton, Alan
APPLICANT: Oustfell, Oustfell,
APPLICANT: Oustfell, Oustfell,
APPLICANT: Moroi, Yoichi
TITLE OF INVENTION: CONUUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
FILE REFERENCE: 11746/46002
CURRENT APPLICATION NUMBER: US/10/053,498B
CURRENT FILING DATE: 2002-01-17
PRIOR APPLICATION NUMBER: 08/961,707
PRIOR APPLICATION NUMBER: 08/961,707
NUMBER OF SEQ ID NOS: 321
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 183
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                                                                                                                                                       TYPE: PRT;
CRGANISM: Artificial Sequence
FEATURE:
JUTHER INFORMATION: peptide in ml3 coliphage
US-10-053-520-195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: peptide in m13 coliphage US-10-053-498B-183
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Job time : 140 secs
              PRIOR APPLICATION NUMBER: 08/961,707
PRIOR FILING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 321
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 195
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 183, Application US/10053498B Publication No. US20030194409A1 GENERAL INFORMATION:
2002-10-01
                                                                                                                                                                                                                                                                                                    71.1%;
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                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 33.33
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 2 YWXXXW 7
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2 HWQMLW 7
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2 HWWDWW 7
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

January 3, 2005, 17:01:32 ; Search time 38 Seconds (without alignments) 17.724 Million cell updates/sec

US-10-046-922-67

1 GYWXXXW 7 Perfect score:

Scoring table: Sequence:

BLOSUM62DX Gapext 0.5

Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

457

Minimum DB seq length: 0
Maximum-DB-seq-length: 777

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

gut pentapeptide cerebellar degener
dermorphin (Trp-4,
T-cell receptor be
R-cell receptor be
R-cell receptor be
R-cell receptor be
gullulanase (RC 3,
R-CH-related neuro
cholecystokinin-5 neuropeptide - sea Ig heavy chain CRD T-cell receptor be alcohol dehydrogen dnaA protein - Pse dihydrofolate redu treell receptor be T-cell receptor be pev-kinin 2 - pena locustakinin - mig hypothetical protein glycoprotein compo SUMMARIES PT0728 PT0629 PT0532 PN0649 A34626 A32516 PT0281 PT0308 PT0729 PT0580 S66195 B34835 PT0726 PD0028 PT0519 F41946 461068 Query Match Length Score Result No. 9876987698769898989989

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Gaps

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Score 17; DB 2; Length 6; Pred. No. 2.8e+05; 4; Mismatches 0; Indels

Query Match
Best Local Similarity 20.0%;
Matches 1; Conservative 4

2 YWXXX 6

ŝ 셤 RESULT S21230

A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-6 < CHE>

ᇊ	T-Cell receptor be T-Cell receptor be T-Cell receptor be	T-cell receptor be T-cell receptor be glucuronosyltransf	major fat-globule pev-kinin 1 - pena triacylqlycerol li	neuromodulatory pe neuromodulatory pe neuromodulatory pe	tubulin beta-3 cha venom heptapeptide
PH1602 PT0526	PT0628 PT0642 PT0722	PT0688 PT0586 PX0008	B48394 PD0029 S57274	S33244 S33245 S33246	S33567 A58512
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36.8	36.8 36.8 36.8	36.8 36.8	36.8 36.8	36.8 36.8	36.8
14	1 1 1	7 7 7	7 7 7	4 4 4	14
30	3 3 3 4 3 3	35 37	338 409	41 42 43	444

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Gispecies: Anguilla japonica (Japanese eel)
C;Species: Anguilla japonica (Japanese eel)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
C;Accession: JH0253
C;Accession: JH0253
Biochem. Biophys. Res. Commun. 180, 828-832, 1991
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.
A;Reference number: JH0253; MUID:92062113; PMID:1953755
A;Accession: JH0253
A;Molecule type: protein
A;Residues: 1-5 <4055
A;Accession: JH0253
A;Accession: JH0253
A;Accession: JH0253
A;Accession: JH0253
A;Accession: This peptide increased basal tone of the circular muscle of the esophagogastr;
and of the circular muscle of the gastro-intestinal junction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CjAccession: B35640
R;Chen, Y.T.; Rettig, W.J.; Yenamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner, J.B Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990
A;Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal mar? A;Reference number: A35640; MUID:90222173; PMID:2326268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cerebellar degeneration-related protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 24-Jun-1993
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                                     - Japanese eel
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Best Local Similarity
Matches 2; Conserv
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1 GFWNK 5
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                              gut pentapeptide
C;Species: Anguil
JH0253
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pullulanase (EC 3.2.1.41) - Bacillus sp. (strain S-1) (fragment)
C;Species: Bacillus sp.
C;Species: Bacillus sp.
C;Accession: PN0649
R;Kim, C.H.; Choi, H.I.; Lee, D.S.
Bjosci. Blockechnol. Blochem. 57, 1532-1637, 1993
A;Title: Purification and biochemical properties of an alkaline pullulanase from alkaloph A;Reference number: PN0649; MUID:94080025; PMID:7764261
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                                                                                                                                                                                                  R,Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A,Fittle: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A,Reference number: PT0509; MUID:91277601; PMID:1711558
A,Recession: PT0629
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J. Exp. Med. 174, 115-124, 1991
A.Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A; Reference number: PT0509; MUID:91277601; PMID:1711558
A; Accession: PT0532
                                                                                                                   C.Species: Mus musculus (house mouse)
C.Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C.Accession: PT0629; PT0528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-cell receptor beta chain V-D-J region (100-4AJ) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0532
                                                                                          :-cell receptor beta chain V-D-J region (100-2AH) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-6 <FEE>
A;Experimental source: newborn thymus, strain BALB/c, clone 100-2AH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-6 <FE2>
A;Experimental source: adult thymus, strain BALB/c, clone 100-4AB
C;Keywords: T-cell receptor
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Pred. No. 2.8e+05;
0; Mismatches 1; Indels
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A;Residues: 1-6 <FBE>
A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor
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Similarity 50.0%;
2; Conservative
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Best Local Similarity 66.7%;
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                      A;Status: translation not shown A;Molecule type: mRNA
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A;Status: translation not shown
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Best Local Similarity
Matches 2; Conserv
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dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment)
C;Species: Phyllomedusa bicolor (two-colored leaf frog)
C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 18-Aug-2000
C;Accession: S21230
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, GFBS Lett. 302, 151-154, 1992
A;Title: Identification and characterization of two dermorphins from skin extracts of A;Reference number: S21152; MUID:92339502; PMID:1633846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: F4-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: F4-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Febrence number: A41946; MUID:92049316; PMID:1658619
A;Accession: F41946
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A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PTG509; MUID:91277601; PMID:1711558
                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 1-7 <MIG>
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology
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C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0728
R;Peeney, A.J.
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                                                                                                                                                                                                                                                                                                                                                                                      Score 17; DB 2; Length 7; Pred. No. 2.8e+05; 4; Mismatches 0; Indels
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A;Residues: 1-7 cFEB.
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor
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Pred. No. 2.8e+05; 2; Mismatches 1
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20.0%;
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Best Local Similarity 20..
Lag 1; Conservative
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Best Local Similarity 40.0
Matches 2; Conservative
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A; Status: preliminary
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Gaps

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Gaps

Gaps

Query Match

Matches

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Syramida, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and jc.
A;Reference number: Pr0222; MUID:91108337; PMID:1899102
A;Reference procession: Pr0281
A;Rolcoule type: DnA
A;Residues: 1-5 < YXM>
A;Residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and jc
A;Reference number: PT0222; MUID:91108337; PMID:1899102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain CRD3 region (clone 6-88) - human (fragment)
C.Species: Momo sapiens (man)
C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C.Accession: PT0308
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0640; PT0665; PT0729
                              A,Accession: A60803
A,Molecule type: protein
A,Rosidues: 1-5 <GRA>
C,Residues: 1-5 <GRA>
C,Reywords: anidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;5/Modified site: amidated carboxyl end (Trp) #status experimental
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Reference number: A60803; MUID:88222764; PMID:2897223
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Pred. No. 2.8e+05;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                          36.8%; Score 14; DB 2; I 25.0%; Pred. No. 2.8e+05; Live 3; Mismatches 0;
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Similarity 25.0%; Pred. No. 2.8e+05;
1; Conservative 3; Mismatches 0;
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A,Molecule type: DNA
A,Residues: 1-5 < YAM>
A,Experimental source: B lymphocyte
C,Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Keywords: heterotetramer; immunoglobulin
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A,Residues: 1-5 <SHI>
C,Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecystc C;Superfamily: gastrin
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide
P;5/Modified site: amidated carboxyl end (Phe) #status experimental
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NAlternate names: CK-5.
NAlternate names: CK-5.
C;Alternate names: CK-5.
C;Alternate names: CK-5.
C;Accession: A32516
R;Shively, J: Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.
Am. J. Physiol. 252, G272-G275, 1987
A;Title: CK-5: sequence analysis of a small cholecystokinin from canine brain and intes
A;Reference number: A32516; MUID:87153871; PMID:3826354
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Kigraff, D.; drimmelikhuijzen, C.J.P.
Brain Res. 442, 354-358, 1988
A;Title: Isolation of <Glu-Ser-Lu-Arg-Trp-NH-2, a novel neuropeptide from sea anemones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        jKuroki, Y.; Kanda, T.; Kubota, I.; Fujiaawa, Y.; Ikeda, T.; Miura, A.; Minamitake, iochem. Biophys. Res. Commun. 167, 273-279, 1990
;Title: A molluscan neuropeptide related to the crustacean hormone, RPCH. ;Reference number: A34626; MUID:90179762; PMID:2310394
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;Species: Fusinus ferrugineus (ferruginous spindle)
;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
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   C; Keywords: glycosidase; hydrolase; polysaccharide degradation
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                                                                 Score 15; DB 2; I
Pred. No. 2.8e+05;
4; Mismatches 1;
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Local Similarity 16.7%;
les 1; Conservative 4
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Best Local Similarity 25.0
Matches 1; Conservative
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1 FLNMSW 6
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RESULT 10

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Query Match

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R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Exp. Med. 174, 115-124, 1991
A; Fitle: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A; Reference number: PT0509; MUID:91277601; PMID:1711558
A; Accession: PT0640
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 1-5 < FEE>
A; Experimental source: newborn thymus, strain BALB/c, clone 120-1J
A; Accession: PT0685
A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-5 < FEE>
A; Accession: PT0729
A; Accession: PT0729
A; Accession: PT0729
A; Accession: PT0729
A; Residues: 1-5 < FEE>
A; Experimental source: newborn thymus, strain BALB/c, clone 135-1AG
C; Keywords: T-cell receptor
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PT0580
T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0580
S;Feeney, A.J.
SEXD. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0580
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/C
C;Keywords: T-cell receptor
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Job time : 39 secs
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Best Local Similarity 25.0
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1 ASSW 4
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                                                                                                                             January 3, 2005, 17:09:38; Search time 185 Seconds (without alignments) 21.771 Million cell updates/sec
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(c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                               1825181 seqs, 575374646 residues
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BRHP_CONIM
TPFY_PACDA
TPFY_PACDA
TPFY_PACDA
WWA1_ACHFU
WWA3_ACHFU
WWA3_ACHFU
095945
04923
04923
086L00
08GL00
08GL00
08GL00
08GRMS9
08JE81
BPPY_BOTIN
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RE32 LITRU
ACH1 ACHFU
OCP1 OCTMI
FAR5 HIRME
UNO6 PINPS
GRWM HUMAN
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ASCL ALLAS
FAR3 HAECO
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Maximum Match 100%
Listing first 45 summaries
                                                                                      OM protein - protein search, using sw model
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2: uniprot_trembl:*
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38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UniProt 02:*
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                    Copyright
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Maximum DB sequength@ 76.
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Query
Match 1
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Perfect score:
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32 8 21.1 7 1 FAR3 PANRE P99025 34 8 21.1 7 1 GRPP_MOUSE P99025 35 8 21.1 7 2 D93482 P82445 36 8 21.1 7 2 P82445 P8245 37 8 21.1 7 2 P82445 P8246 39 7 18.4 4 1 FAR1_ANTEL P83900 40 7 18.4 4 1 FAR1_ANTEL P83900 41 7 18.4 4 1 FAR1_ANTEL P83900 42 7 18.4 4 1 FAR1_ANTEL P83900 43 7 18.4 5 1 PARP_ANTER P8280 44 7 18.4 5 1 PARP_ANTER P8280 45 7 18.4 5 1 PARP_ANTER P8280 45 7 18.4 5 1 PARP_ANTER P8280 46 7 18.4 5 1 PARP_ANTER P8280 47 18.4 5 1 PARP_ANTER P8280 48 7 18.4 5 1 PARP_ANTER P8280 49 7 18.4 5 1 PARP_ANTER P82805 45 7 18.4 5 1 PARP_ANTER P82805 45 7 18.4 5 1 PARP_ANTER P82805 45 7 18.4 5 1 PARP_ANTER P82806 45 7 18.4 1 STANDARD; PRT; S.A.  ALIGNMENTS  DT 01-OCT-1994 (Rel. 30, CTeated) DT 01-OCT-19090907; PUNDAG-7533108; DT 01-OCT-19090907; PUNDAG-7533108; DT 01-OCT-19090907; PUNDAG-7533108; DT 01-OCT-19090907; PUNDAG-753	65.8%; Score 25; DB 1; 40.0%; Pred. No. 1.8e+06; ative 3; Mismatches 0	JOCTMI STANDARD; PRT; 4 AA.  OCP3 OCTMI STANDARD; PRT; 4 AA.  P86849; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 44, Last sequence update) 28-FEB-2004 (Rel. 44, Last sequence update) 65-JUL-2004 (Rel. 44, Last sanctation update) 65-JUL-2004 (Rel. 44, Last sanctation update) 65-JUL-2004 (Rel. 47, Last sanctation of cotopus) 65-JUL-2004 (Rel. 47, Last sanctation) 65-JUL-2004 (Rel.
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InterPro; IPR000433; Znf_ZZ
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Matches 1; Conserv
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E101_LITRU
ID E101_LITRU
AC P82096;
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LOK1_LOCMI
ID _LOK1_LOCI
AC P41491;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

BMBL; BC005857; AAH05857.3; -.
BMBL; BC005857; AAH05857.3; -.
BM GO; GC0:0019901; F:protein kinase binding; ISS.
BM GO; GC0:0042169; F:Sprotein kinase binding; ISS.
BM GO; GC0:0041130; F:ubiquitin binding; ISS.
BM GO; GC0:0041130; F:ubiquitin binding; ISS.
BM GO; GC0:0041310; F:ubiquitin binding; ISS.
BM GO; GC0:004142; P:intracellular signaling cascade; ISS.
BM GO; GC0:004104; P:protein localization; ISS.
BM GO; GC:0004112; P:regulation of transcription from P. .; ISS.
BM GO; GC:0004112; P:regulation of L'kappaB cas. .; ISS.
BM GO; GC:0006500; P:response to stress; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MILL Riamer R.D., Colline F.S., Magner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.H., Rubin G.M., Heiseh F.,

Diatchenko L., Marusina K., Parmer A.H., Rubin G.M., Heiseh F.,

Diatchenko L., Joanes M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Rapleton M., Saares M.B., Ponaldo M.F., Casavant T.L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitting M., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                       ö
                                            than Ocp-3.
-!- SUBCELLULAR LOCATION: Secreted.
-!- PTM: Ocp-4 has D-Ser instead of L-Ser.
-!- MASS SPECTROMETRY: MW-395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.
                                                                                                                                                                                                         Gaps
             -1- FUNCTION: Cardioactive; has both positive chronotropic and inotropic effects on the heart. Ocp-4 is a 1000 time less active
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                         ö
                                                                                                                                                                                                       1; Indels
                                                                                                                                                                          Length 4;
                                                                                                          D-amino acid, Direct protein sequencing; Hormone.
MOD RES 2 D-serine (in form Ocp-4).
SEQÜENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                        42.1%; Score 16; DB 1; I 50.0%; Pred. No. 1.8e+06; tive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17,
Peptides 21:623-630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO: 0019901; F: protein
GO; GO: 0042169; F: SH2 doma
GO; GO: 0042169; F: SH2 doma
GO; GO: 0016197; P: ubiquiti:
GO; GO: 0007242; P: intracel
GO; GO: 0004144; P: protein
GO; GO: 0004142; P: regulati:
GO; GO: 00043122; P: regulati:
GO; GO: 0006950; P: regulati:
InterPro; IPR000449; UBA.
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                                                                                                                                                                                                       2; Conservative
                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Matches
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Q9BRY4
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Gaps
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Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
Webtides from the skin glands of the Australian buzzing tree frog
Litori electrica. Comparison with the skin peptides from Litoria
rubella.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Litoria rubella (Desert tree frog).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Pelodryadinae; Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rubella.";
Must. J. Chem. 52:639-645(1999).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
Amidation; Amphibian defense peptide; Direct protein sequencing.
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Locustakinin (Migratory locust).
Locusta migratoria (Migratory locust).
Eukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Reopters; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Locusta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Corpora cardiaca;
MEDLINE=92262851; PubMed=1585017;
Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
de Loof A.;
                                                                                                                                                                                                                   Score 16; DB 2; Length 7; Pred. No. 1.8e+06; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.5%; Score 15; DB 1; Length 6; 20.0%; Pred. No. 1.8e+06; Live 4; Mismatches 0; Indels
                                                                                                                                                                   737728769DDDD6F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 AA; 792 MW; 6683704772C9A000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 AA.
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F
                                                                                 PROSITE; PS50030; UBA; 1.
PROSITE; PS01357; ZF ZZ 1; UNKNOWN_1.
SEQUENCE 7 AA; 779 MW; 737728769DI
                                                                                                                                                                                                                   h 42.1%;
Similarity 66.7%;
2; Conservative
Pfam; PF00569; ZZ; 1.
SMART; SM00165; UBA; 1.
SMART; SMO0291; ZnF_ZZ; 1.
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Best Local Similarity
Matches 2; Conserv
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-i- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI; RANGE=1-7; NOTE=Ref.1. GO; GO:0005576; C:extracellular; NAS. GO; 00:0005576; P:negative regulation of smooth muscle contra. ..; NAS. Amidation; Amphibian defense peptide; Direct protein sequencing;
                                                                                                                                                  SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
                                                                                                                                                                                                                                                                Submitted (SEP-2002) to Swiss-Prot.
-!- FUNCTION: Myoactive. Has selective relaxing activity on vascular smooth muscle.
                                                                                                                                                                                                                                   characterization, pharmacological activity and cloning of precursor
                                                 Pachymedusa dacnicolor (Giant mexican leaf frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
                                                                                                                                                                                                 Chen T.B., Orr D.F., Shaw C., "Pachymedusa dacnicolor tryptophyllin-1 (PdT-1): structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14; DB 1; Length 7; Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 7 Proline amide.
7 AA; 794 MW; 7772D37DC7776350 CRC64;
   28-FEB-2003 (Rel. 41, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Tryptophyllin-1 (PdT-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydroxyproline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tryptophyllin 5.1.
Litoria rubella (Desert tree frog)
                                                                                                    Phyllomedusinae; Pachymedusa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.8%;
25.0%;
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                                                                                                                                                                                   TISSUE=Skin secretion;
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Matches 1; Conserv
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2 PPAW 5
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P82065;
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MOD RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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TY51_LITRU
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                                                   stimulation
in Malpighian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A novel post-translational modification involving bromination of tryptophan. Identification of the residue, L-6-bromotryptophan, in peptides from conus imperialis and Conus radiatus venom.";
J. Biol. Chem. 272:4689-4689(1991).
-I- FUNCTION: Does not elicit gross behavioral symptoms when injected centrally or peripherally in mice.
-I- SUBCELMULAR LOCATION: Secreted.
-I- TISSUE SPECIFICITY: Expressed by the venom duct.
-I- MASS SPECIFICITY: Expressed by the venom duct.
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Craig A.G., Jimenez E.C., Dykert J., Nielsen D.B., Gulyas J., Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M., McIntosh J.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acid.
                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                               36.8%; Score 14; DB 1; Length 6; 25.0%; Pred. No. 1.8e+06; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                             -!- SUBCELLULAR LOCATION: Secreted.

PIR; A61068; A61068.

Andidation; Direct protein sequencing; Neuropeptide.

MOD RES

SEQUENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6'-bromotryptophan.
Cysteine amide.
6EA37DC6D87EA6B0 CRC64;
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Amidation, Bromination, Direct protein sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                  7 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97184108; PubMed=9030520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conus imperialis (Imperial cone)
                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 41, Created)
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                                                                                                                                                                                                                                   1; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                4 XXXW 7
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TPFY PACDA
ID TPFY PA
AC P83455,
DT 28-FEB-
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Gaps

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Indels

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TISSUE-Skin secretion;

A TISSUE-Skin secretion;

A TISSUE-Skin secretion;

A TISSUE-Skin secretion;

A Tyler M.J. Wallace J.C.;

Tyler M.J. Wallace J.C.;

Tiltoria rubella. The skin peptide profile as a probe for the study of evolutionary trends of amphibians.";

L Aust. J. Chem. 49:955-963(1996).

- I FUNCTION: May act as a neuromodulator or neurotransmitter.

- SUBCELLULAR LOCATION: Secreted.

- SUBCELLULAR LOCATION: Secreted.

- TISSUE SPECTROMETRY: Expressed by the skin dorsal glands.

- MASS SPECTROMETRY: MW=965; METHOD=FAB; RANGE=1-7; NOTE=Ref. 1.

- MASS SPECTROMETRY: MW=965; METHOD=FAB; Direct protein sequencing;
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae; Pelodryadinae; Litoria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pyrrolidone carboxylic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arginine amide.
                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
7 AA.
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25.0%;
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Matches

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Matches

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Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Sigmurethra; Achatinoidea; Achatinidae; Achatina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUB=Ganglion;
MEDLINE=93265912; PubMed=8495720;
Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
"Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the African giant snail, Achatina fulica.";
PEBS Lett. 323:104-108 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=D273-10B;
MEDLINE=81069885; PubMed=6254986;
Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
"Assembly of the mitochondrial membrane system: Structure and
nucleotide sequence of the gene coding for subunit 1 of yeast
cytochrome oxidase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14; DB 1; Length 7;
Pred. No. 1.8e+06;
3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amidation; Direct protein sequencing; Neuropeptide.

MOD RES 7 7 Tryptophan amide.

SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;
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7 AA; 859 MW; 75B7232362CDC460 CRC64;
                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
WMamide-3.
                                                                                                                                                      7 AA.
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                                                                                                                                                                                                                                                                                                            Achatina fulica (Giant African snail).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biol. Chem. 255:11927-11941 (1980).
EMBL; V00694; CAA24066.1; --
GO; GO:0005739; C:mitochondrion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 36.8%;
Similarity 25.0%;
1; Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inside intron 5 (Fragment)
                                                                                                                                                        STANDARD;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6530;
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1 WKEM 4
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  |:::
1 WKQM 4
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4 WKLS 7
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SEOUENCE
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                                                                                                     RESULT 11
WWA3_ACHFU
                                                                                                                                                                                    P35921
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Bukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Sigmurethra; Achatinoidea; Achatinidae; Achatina.
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Achatina fulica (Giant African snail).
Ekkaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora; Sigmurethra; Achatinoidea; Achatinidae; Achatina.
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.
TISSUB-Ganglion;
MINDALINE-93265912; PubMed=8495720;
Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
Minakata H., Lada T., Muneoka Y., Kobayashi M., Nomoto K.;
"Wwamide-1., -2 and -3: novel neuromodulatory peptides isolated from ganglia of the African giant snail, Achatina fulica.";
FEBS Lett. 323:104-108(1993)
-!-FUNCTION: Exhibits modulatory effects on the peripheral nervous system. Inhibits activity on a central neuron.
PIR, 533245, S33245.
Amidation; Direct protein sequencing; Neuropeptide.
Amidation, Direct protein sequencing; Neuropeptide.
SEQÜENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;
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"WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the African giant snail, Achatina fulica.";
FEBS Lett. 323:04-108(1993).
PIR; S33246; S33246.
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Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 3; Mismatches 0;
                                                                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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01-JUN-1994 (Rel. 29, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                     7 AA.
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Mismatches
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TISSUE-Ganglion;
MEDLINE-93265912; PubMed=8495720;
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ن
1; Conservative
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WFHR 7
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1 WREM 4
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                                                                                                                                                                                 RESULT 9
WWA1_ACHFU
AC P35919;
DT 01-JUN-1994
DT 01-JUN-1994
DT 01-JUN-1994
DT 05-JUL-2004
DE WWamide-1.
OC Sigmurechra;
OC Sigmurechra;
OX NCBI_TaxID=6
RN [1]
RP SEQUENCE.
RP SEQUENCE.
RR MIDARATA H.,
RT "WAMMIGE-1,
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P35920;
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WWA2 ACHFU
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Gaps

Gapa

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36.8%; Score 14; DB 2; Length 7; 25.0%; Pred. No. 1.8e+06; tive 3; Mismatches 0; Indels

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7 AA; 928 MW; 6337233050437350 CRC64;
                                                                                        1; Conservative
                                           Query Match
Best Local Similarity
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1 WIIK 4
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SEQUENCE
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08GL04;
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"Intra- and interbacterial genetic exchange of Lyme disease spirochete erp genes generates sequence identity amidst diversity.";
D. Mol. Bvol. 57:309-324 (2003).
EMBL; AY142106; AAN17857.1; -.
                                                                                                                                                                                                                                                                                                                                                               TISSUB=Roces,
MEDLINE=91367679; PubMed=1891369;
Laux T., Goldberg NB.;
Laux T., Goldberg R.B.;
with HMG-box proteins.";
Nucleic Acids Res. 19:4769-4769(1991).
                                                                                                                                                                                                                Glycine max (Soybean).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae, Glycine.
NCBI_TaxID=3847;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid group cp32-13.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia
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Mahalingam R., Knap H.T.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF047050; AAC03556.1;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                          01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HMG-1-like protein (Fragment).
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Name=PF-50;
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MEDLINE=22990544; PubMed=14629041;
MEDLINE=2290544; PubMed=14629041;
Stevenson B., Miller J.C.;
"Intra- and interbacterial genetic exchange of Lyme disease spirochete erp genes generates sequence identity amidst diversity.";
J. Mol. Evol. 57:309-324(2003)
EMBL; AY142103; AAN17848.1;
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MEDLINE=22610300; PubMed=12724373;
Miller J.C., Stevenson B.;
"Immunological and genetic characterization of Borrelia burgdorferi
                                                                                                                                                                                                            Plasmid group cp32-5.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
PF-50 protein (Fragment).
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7 AA; 914 MW; 6337244330504310 CRC64;
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tive 3; Mismatches 0;
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Job time : 187 secs
PRT;
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Microbiology 149:1113-1125(2003).
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nes 1; Conservative
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Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 seqs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_23Sep04:* geneseqp1980s:* geneseqp1990s:* Database :

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* 4.0.0.0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Abp53965 VEGFR-3 b	Abp53933 VEGFR-3 b	Aab99759 Rhesus D	Abp53931 VEGFR-3 b	Abp53968 VEGFR-3 b	Abp53932 VEGFR-3 b	Aaw62148 Haemophil	Adj25827 Tyrosine		Aao26093 Fc region	Adj50760 Human ser	Aau93268 Granulocy	Adc99638 Cancer-re			Abb19829 Protein #	Aam55207 Human bra	Abb41036 Peptide #	Aam34810 Peptide #	Abb25111 Protein #	Aam74694 Human bon	Aam61892 Human bra	Abg56478 Human liv	Abg44505 Human pep	Human
	ID	ABP53965	ABP53933	AAB99759	ABP53931	ABP53968	ABP53932	AAW62148	ADJ25827	AAB99769	AA026093	ADJ50760	AAU93268	ADC99638	ABB34417	AAM27898	ABB19829	AAM55207	ABB41036	AAM34810	ABB25111	AAM74694	AAM61892	ABG56478	ABG44505	AA013595
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# ALIGNMENTS

angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; ulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hyportension; post trauma; chronic hepatitis; haemangioma; diabetes; pDGF; platelet derived growth factor. Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; VEGFR-3 binding peptide SEQ ID NO:68. ABP53965 standard; peptide; 8 AA. (first entry) 09-JAN-2003 ABP53965; RESULT 1 ABP53965 

Homo sapiens. Synthetic.

/note= "X is any amino acid"
8 /note= "any amino acid" Location/Qualifiers Misc-difference 4. Misc-difference WO200257299-A2

25-JUL-2002.

16-JAN-2002; 2002WO-IB000099.

17-JAN-2001; 2001US-0262476P.

(LUDW-) LUDWIG INST CANCER RES. (LICN ) LICENTIA LTD.

Kubo H; Alitalo K, Koivunen E,

WPI; 2002-691521/74.

New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.

Claim 22; Page 81; 149pp; English.

The present invention describes an isolated peptide (I) that binds to and

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inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, pancreas, colon, stomach, brast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VBGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and itsrating disorders mediated by the activity of the cell surface receptor VBGFR-3 such as cancer, e.g. brain, lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive, antiidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8 AA;
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ABP53933
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The present sequence represents a peptide capable of binding Rhesus D antibodies (I). Also described in the present invention are: (1) a nucleic acid (II) encoding (II); (2) a vector (III) comprising one or more (III) operably linked to an expression control system: (3) a cell (IV) comprising (II) or (III); (4) preparing (I); (5) identifying (M1) comprising subjecting expression control system: (3) a cell (IV) peptides having immunologic properties of Rhesus D protein epitopes comprising an antibody/antibody fragment recognising an epitope of Rhesus D protein to several panning rounds with a phage display library, and identifying immunogenic peptide sequences which are minotopes which differ in their amino acid sequences of Rhesus D protein, and (6) peptides (V) with immunological sequences of Rhesus D protein epitopes obtained by (M1). (I) is used to manufacture an agent for the diagnosis, therapy or prophylaxis of diseases associated with Rhesus D antigen, e.g. haemolytic disease of the comborn (HDN) or idiopathic thrombocytopaenic purpura (ITP), for the manufacture of an affinity reagent for anti-Rhesus D antified
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liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases. Pypertension, post-trauma, chronic hepatitis, haemanglomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
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                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhesus D antibody binding peptide; Rhesus D; RhD; identification; anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy; prophylaxis; haemolytic disease of the newborn; HDN; ITP; idiopathic thrombocytopaenic purpura; immunoglobulin.
                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                         Length 9;
                                                                                                                                                                                                         ; Score 39; DB 5; Length 9;
Pred. No. 1.7e+06;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhesus D antibody binding peptide SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB99759 standard; peptide; 10 AA.
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                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                 4; Conservative
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GYWWDTWF 9
                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                           present invention
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                                                                                                                                                                   Sequence 9 AA;
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Gaps

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Pred. No. 46; 4; Mismatches Score 39;

5; Length 10; Indels

DB

100.08;

50.0%;

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neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                                                                                                                                    4; Conservative
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GYWLTIWG 9
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Best Local Similarity
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                                                                                         present invention
                                                                                                                                                 Sequence 10 AA;
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ABP53968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidlabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
or removed from body fluids or immunoglobulin preparations. Using (I) as an immunogen to raise anti-Rhesus D antibodies avoids using immunisation with foreign erythrocytes thereby avoiding the risk of transmission of viral diseases like AIDS and hepatitis B
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                                                                                                                                                                                                                                                                       Gaps
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4; Mismatches
                                                                                                                                                                                                            Score 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEGFR-3 binding peptide SEQ ID NO:34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LUDW-) LUDWIG INST CANCER RES
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                                                                                                                                                    Sequence 10 AA;
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ABPS 39
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The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antiidiabetic and valuerary activities, and can be used in gene therapy. Compositions and wethods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
                                                                                                                                          Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; anglogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
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                                                                                                          VEGFR-3 binding peptide SEQ ID NO:73.
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ABP53968 standard; peptide; 10 AA.
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                                                                        (first entry)
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                                                                                                                                                                                                                                                                             sapiens.
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Gaps

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0; Indels

; Score 39; DB Pred. No. 46; 4; Mismatches

100.0%;

4; Conservative

Query Match Best Local Similarity Matches 4; Conserv

|||:::|: GYWLTIWG 9

1 GYWXXXWX

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Length 10;

OB

21.

Haemophilus influenzae tyrosine tRNA synthetase binding peptide

(first entry)

16-SEP-1998

AAW62148;

AAW62148 standard; peptide; 11 AA.

RESULT 7 AAW62148 Identification, ligand; biological activity; target-binding; drug screening; library; inhibitory ligand.

Haemophilus influenzae

Synthetic

WO9819162-A1

07-MAY-1998.

96US-00740671. 97WO-US019638

31-OCT-1997; 31-OCT-1996; (NOVA-) NOVALON PHARM CORP.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antininflamatory, hypotenaive, antidiabetic and valuerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antiidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
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                                                                                                                                                              Gaps
neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a VEGFR-3 binding peptide, which is given in the exemplification of the present invention
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                                                                                                                   Query Match 100.0%; Score 39; DB 5; Length 10; Best Local Similarity 100.0%; Pred. No. 46; Matches 8; Conservative 0; Mismatches 0. Tridale
                                                                                                                                                                                                                                                                                                                                                                                                                                    VEGFR-3 binding peptide SEQ ID NO:35.
                                                                                                                                                                                                                                                                                                                         ABP53932 standard; peptide; 10 AA.
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                                                                                                                                                                                                                              2 GYWXXXWX
                                                                                         Sequence 10 AA;
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A method has been developed for identifying a ligand which mediates the biological activity of a target protein (T) by inhibiting the binding of C (T) to a binding partner. The method comprises: (a) screening a first combinatorial library comprising first member ligands for binding to the target-binding ligands (TBLs), to identifying one or more TBLs; (b) screening a second library comprising second member ligands for the binding of one or more of the TBLs to the target protein, and so obtaining one or more inhibitory ligands; and (C) determining which of the inhibitory ligands can mediate a biological crivity of the target protein. The present sequence represents a potential binding peptide for Haemophilus influenzae tyrosine tRNA synthetase from an example of the present invention. The method can be used for identifying drugs which can mediate the biological activity of a target protein. It can be used to identify the biological activity of a target protein. It can be used to identify the biological activity of a target protein. The method can also be used to identify new throughput screens which are essentially identical for similar and dissimilar targets. Pypassing the need to develop distinct assays for biochemically diverse targets
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying ligands which mediate biological activity of a protein - by identifying target-binding ligands and screening a library for ligands which inhibit target-binding ligand mediated activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        Fowlkes DM, Kay BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-272389/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11 AA;
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present invention

Sequence 10 AA

Rhesus D antibody binding peptide; Rhesus D; RhD; identification; anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy; prophylaxis; heamolytic disease of the newborn; HDN; ITP; cyclic; diopathic thrombocytopaenic purpura; immunoglobulin; circular.

Location/Qualifiers

Disulfide-bond

EP1106625-A1.

13-JUN-2001.

sapiens.

Ношо

Synthetic.

Rhesus D antibody related peptide #5.

21-SEP-2001 (first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mediate the biological activity of target protein via inhibition of the binding of target protein to a binding partner ligand comprising screening first combinatorial library having first member ligands for binding to target protein to identify target-binding ligand(s). The method is useful for identifying ligands that can mediate the biological activity of target proteins via inhibition of the binding of target proteins via inhibition of the binding of target the natural binding partner ligand. The invention does not require that the natural binding partner he used as reagent. The need for the natural binding partner sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identification of ligand that can mediate biological activity of target protein, comprises screening first combinatorial library having first member ligands for binding to target protein to identify target-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method of identifying a ligand that can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                ligand identification; peptide library;
complementary combinatorial library; tyrosine tRNA synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 8; Length 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hyde-Deruyscher RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                  Tyrosine tRNA synthetase binding peptide #21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 39; DE pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; SEQ ID NO 87; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Frelinger JA,
                                                                                               ADJ25827 standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                           96US-00740671.
97WO-US019638.
98US-00050359.
                                                                                                                                                                                                                                                                                                                                                98US-00069827
                                                                                                                                                        20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kay BK,
               |||:::|:
GYWWPDWG 8
GYWXXXWX 8
                                                                                                                                                                                                                                                                                                                                                                                                                                     (KARO-) KARO BIO AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-068186/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GYWXXXWX 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                          31-OCT-1996;
31-OCT-1997;
31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                30-APR-1998;
                                                                                                                                                                                                                                                                                       US6617114-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fowlkes DM,
                                                                                                                                                                                                                                                                                                                   09-SEP-2003
                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                             ADJ25827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ligand(s)
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Novel peptides capable of binding Rhesus D antibodies are used to manufacture an agent for the diagnosis, therapy or prophylaxis of diseases associated with Rhesus D antigen, e.g. hemolytic disease of the

Fisch I;

Hofmann A,

Miescher S,

WPI; 2001-383568/41

(ZLBB-) ZLB BIOPLASMA AG

99EP-00122858. 99EP-00122858

17-NOV-1999; 17-NOV-1999;

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The present invention describes peptides capable of binding Rhesus D antibodies (1). Also described in the present invention are: (1) a nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more (II) operably linked to an expression control system; (3) a cell (IV) comprising (II) or (III); (4) preparing (I); (5) identifying (M1) peptides having immunologic properties of Rhesus D protein epitopes comprising subjecting an antibody/antibody fragment recognising an epitope of Rhesus D protein to several panning rounds with a phage display library, and identifying immunogenic peptide sequences which are minotopes which differ in their amino acid sequence from the amino acid sequences of Rhesus D protein; and (6) peptides (V) with immunological properties of Rhesus D protein epitopes obtained by (M1). (1) is used to manufacture an agent for the diagnosis, therapy or prophylaxis of diseases associated with Rhesus D antigen, e.g. haemolytic disease of the newborn (HDN) or idiopathic thrombocytopenic purpura (ITP), for the manufacture of an affinity reagent for anti-Rhesus D antibodies purified or removed from body fluids or immunoglobulin perparations, using immunications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an immunogen to raise anti-Rheeus D antibodies avoids using immunisation with foreign erythrocytes thereby avoiding the risk of transmission of viral diseases like AIDS and hepatitis B. The present sequence represents an anti-Rhesus D (RhD) antibody related peptide which is used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 8; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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장.: 원
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AAB99769 standard; peptide; 12 AA.

AAB99769

RESULT 9
AAB99769
ID AAB9
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AC AAB9

GYWWPDWG

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The invention relates to a method of evaluating sample by providing a soluble serum protein (I), one or more compounds physically associated with (I), and a (I)-binding agent that comprises a peptide that comprises a peptide that comprises a peptide that to form a complex including one or more compounds physically associated with (I), separating the complex from one or more compounds physically associated compounds. The sample comprises blood or serum, or is obtained from a bippy. The sample comprises blood or serum, or is obtained from a compounds. The method is useful for detecting modulators that modulate interaction of serum protein-binding compound and serum protein and lor identifying binding ligands for serum protein. The present cand for identifying binding ligands for serum protein. The present sequence represents a serum albumin-binding peptide identified using the method of the invention.
                                                                                                                                                                          Evaluating sample comprising soluble serum protein by forming complex comprising serum protein and physically associated compounds using peptide ligand that specifically binds with proteins, which is separated and evaluated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Granulocyte-colony stimulating factor receptor binding peptide #74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G-CSFR; granulocyte-colony stimulating factor receptor; cytokine; haematopoietic growth factor; neutrophil proliferation; AIDS; neutrophil differentiation; acquired immunodeficiency syndrome; chemotherapy-induced neutropaenia; community acquired pneumonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mceowen-Merrill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 39; DB 8; Length 13;
50.0%; Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              depressed neutrophil count; immunostimulant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 60;
4; Mismatches
                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 297; 191pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU93268 standard; peptide; 16 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUL-2001; 2001WO-US023046.
                14-JUN-2002; 2002US-0388642P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JUL-2000; 2000US-00620091.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLAX ) GLAXO GROUP LTD
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                                                                                               Dawson BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 | | | ::: | :
1 GYWCNVWG 8
                                                                                                                                       WPI; 2004-082161/08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                        (DYAX-) DYAX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13 AA
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Schatz PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                               Sato AK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
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or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel isolated polypeptides comprising a sequence that binds an immunoglobulin Fc region. The polypeptides are useful as binding molecules for detecting, isolating or purifying immunoglobulin Fc-region polypeptides present in a solution, e.g. whole blood, plasma or transgenic milk. The Fc-region binding polypeptides are also useful for regulating or preventing an antibody response, or for increasing the half-life and over all stability of a therapeutic or diagnostic compound that is administered to or enters the circulatory system of an individual. This sequence represents an Fc region binding
                                                                                                                                       Immunoglobulin Fc region; binding; whole blood; plasma; transgenic milk; antibody response; half-life; stability; circulatory system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isolating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            Potter MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptides, useful as binding molecules for detecting, purifying immunoglobulin Fc-region polypeptides present in a for regulating or preventing an antibody response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Ransohoff TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human serum albumin binding peptide, Seq ID No 297
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4; Mismatches
                                                                                               Fc region binding peptide SEQ ID No 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ley AC, Stochl M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ50760 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 76; 152pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.08;
                                                                                                                                                                                                                                                                                                                      18-APR-2002; 2002WO-US012492.
                                                                                                                                                                                                                                                                                                                                                             18-APR-2001; 2001US-0284534P
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                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide of the invention
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                                                                                                                                                                                                                                         WO200286070-A2
                                                                                                                                                                                                 Unidentified.
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                                                          03-APR-2003
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                                                                                                                                                                                                                                                                                31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                            Rondon IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                    AA026093
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RESULT 11 ADJ50760

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cytostatic; cancer; gene therapy; DGI-2; DGI-5; DGI-7; DGI-9; Hras; leptin; VEGF; vascular endothelial growth factor receptor; VEGF-R1; VEGF-R2; VEGF-R3; FLT1; FMS-related tyrosine kinase 1; FLK1; KDR; kinase insert domain protein receptor; EGFR; epidermal growth factor; FGFR1; fibroblast growth factor; Tie-1.
                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                             Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                   WO2003035839-A2
                                                                                                                                                                                                                                                                                                                     01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                        Unidentified
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Selecting target and target binder pairs for preparing a composition for treating cancer by mixing in a reaction vessel phage expressing biological targets and phage expressing target binders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          binder pairs comprising mixing in a reaction vessel phage expressing biological targets and phage expressing target binders, each having distinguishable selection markers and selecting target and target binder pairs based on the selection markers. The molecules of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             demonstrate cytostatic activity whilst the method may be useful for selecting target and target binder pairs for preparing a composition for treating cancer. Furthermore, the method may be utilised during gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapy procedures. The current sequence is that of the cancer-related Tiel-binder peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel method of selecting target and target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 39; DB 7; Length 25
50.0%; Pred. No. 1.2e+02;
ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                               Spruyt M, Dedova O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 26; SEQ ID NO 476; 172pp; English.
                                                                                                                                                                                                                    (DGIB-) DGI BIOTECHNOLOGIES INC
                                                                                             24-OCT-2002; 2002WO-US034021.
                                                                                                                                                            24-OCT-2001; 2001US-0345471P.
                                                                                                                                                                                                                                                                                                           Prendergast J, Goldstein N;
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                                                                                                                                                                                                                                                                               Brissette R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Best Local Similarity 50.0
Matches 4; Conservative
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6 GYWGELWG 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25 AA;
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                                                                                                                                                                                                                                                                            Pillutla RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2002
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                                     01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB34417;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                          The invention relates to compounds comprising a peptide chain approximately 6 to 40 amino acids in length that binds to granulocytecolony stimulating factor receptor (G-CSR). The compounds contain colony stimulating factor receptor (G-CSR). The compounds contain and the generic sequences XV 1XV 2XV 3XV 4XV 5XV 6XV C7XV 8 (where XV 1 = C = L, A or V; XV 2 = R, A, L, M, R, E, G, D, Q or S; XV 6 = E or V; XV 7 = A or O; and XVI 3 = R, M, H, E Or L) and XVI 1XVI 2XVI 3XVI 4XVI 5 = R, V XV 7 = A or O; and XVI 3 = R, Y Y Y 1 = A, E Or O; XVI 3 = R, F or V; XV 7 = R, V M, N, O, M, R, D, I, S or E; XVI 3 = R, Or V; XV 6 = E, D, T, O, R or A, XVI 7 = R, W, K, L, S, A or O; XVI 8 = R or C i and XVI 9 = W, G or R). The compounds are used for treating conditions controped pneumonia. The compounds are useful as in vitro as tools for understanding the biological role of granulocyte-colony stimulating contropid proliferation and differentiation), including evaluation of factor (G-CSF a haematopoietic growth factor and cytokine that stimulates contropid proliferation and differentiation), including evaluation of metropidil proliferation and differentiation), including evaluation of metropidil proliferation and differentiation), including evaluation of calls, itsed cells, in biological fluid, in tissue homogenates or in purified natural biological fluid, in tissue homogenates or in purified activated cell sorting (FACS), Western blotting or enzyme-linked calls, instead adjecase that would benefit from the ability confidence as a commercial research reagent for various medical and calls expressing G-CSFR on the cell surface (or inside permeabilised colls expressing G-CSFR and allease that would benefit from the ability colon decided by the receptor and colon activation of the invention of the invention of the invention of colls expressing G-CSFR and alleases of biological activities mediated by the receptor and colon activation of the invention G-CSFR. The present sequence is a G-CSFR binding peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                           Novel compounds, useful for treating depressed neutrophil count, comprise peptide chains of approximately 6 to 40 amino acids in length that bind to granulocyte-colony stimulating factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%; Pred. No. 74; ive 4; Mismatches
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                                                                                                                                                                                 Claim 4; Page 53; 90pp; English.
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WPI; 2002-329382/36
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1 GYWCDPWT
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Gaps

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Length 25;

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Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                 Peptide #1923 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                   Rank DR;
ABB34417 standard; peptide; 29 AA.
                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                   Chen W,
                                                                                                                                                         2000US-0207456P.
2000US-00608408.
2000US-00632366.
                                                                                                                                                                                                 2000GB-00024263
                                                                                                                                                                                 2000US-0234687P
                                                                                                                                                                                                                                   Hanzel DK,
                                                                                                                                                         26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                          03-AUG-2000;
                                                                                                                                                                                                  04-OCT-2000;
                                                                                                                                                                                   21-SEP-2000;
                                                                                                                                                                                                                                   Penn SG,
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing
                                         Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide #1935 encoded by probe for measuring placental gene expression.
                                                                                   Claim 27; SEQ ID NO 27052; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                            100.0%; Score 39; DB 4; Length 29; 50.0%; Pred. No. 1.3e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID NO 28167; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W, Rank DR,
                                                      gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM27898 standard; protein; 29 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0263468.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023458P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US000663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                           4; Conservative
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17 GYWQLHWM 24
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                                                                                                                                                                                                                                                                                                                                        GYWXXXWX 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488897/53
            WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                   Sequence 29 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157272-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM27898;
                                                                                                                                                                                                                                                                              Query Match
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The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of

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Gaps ö

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                                               Length 29;
                                                                        0; Indels
                                               100.0%; Score 39; DB 4;
50.0%; Pred. No. 1.3e+02;
ive 4; Mismatches 0;
                                                                                                                                                            3, 2005, 16:27:23
                                                                         Conservative
human genetic disorders
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Job time: 91.88 secs
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                                               Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                1 GYWXXXWX
                         Sequence 29 AA
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 87:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202) 628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 81, Appl
Sequence 7620, Ap
Sequence 10, Appl
Sequence 12, Appl
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3, Appli
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Sequence 4, Appli
Sequence 35277, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 87, Appl
Sequence 81, Appl
                                                                                    January 3, 2005, 16:19:47; Search time 23.04 Seconds (without alignments) 23.027 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
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Sequence 6
Sequence 6
Sequence 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-620-091-81

US-09-502-653-10

US-09-502-653-10

US-09-610-906-12

US-09-108-196-15791

US-09-128-191A-15791

US-09-128-191A-2641

US-09-252-991A-2641

US-09-252-991A-2188

US-09-107-532A-6868

US-09-252-991A-18697

US-09-252-991A-18697

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US-09-252-991A-18697

US-09-252-991A-18697

US-09-253-991A-18697

US-09-270-676-60715

US-09-270-676-60715

US-09-270-76-60715

US-09-270-76-60715

US-09-2710-76-60715

US-09-2710-76-60715

US-09-2710-76-60715

US-09-2710-76-60715

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US-09-2710-76-60715

US-09-2710-76-76-733

US-09-2710-76-783
                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                      478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                      ABLOSUM62DX
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Maximum DB seq length: 200000000
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39
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No.
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2, 494, A 2, 49pli 8052, Ap 8052, Ap 4052, Ap 34, Appl 1893, Ap 4308, Ap 4308, Ap 4308, Ap 4572, Ap 61294, A 61294, A		
Sequence Seq	IBRARIES	
US-09-270-767-50494 US-09-112-248-2 US-09-489-039A-8752 US-09-248-796A-20388 US-09-245-937A-34 US-09-543-681A-6323 US-09-543-681A-6324 US-09-543-681A-6324 US-09-248-796A-16589 US-09-270-767-61294 US-09-270-767-61294 US-09-270-767-61294 US-09-270-767-61294 US-09-270-767-61294 US-09-270-767-61294 US-09-270-767-61294 US-09-794-5298-8 US-09-794-5298-8	GNMENTS  Bin P  TION OF DRUGS USING ARY COMBINATORIAL L MARK, P.L.L.C. N.W., Sulte 300  #1.0, Version #1.  69,827A  690,359  790,359  7740,671	KEGLEIKALION NOMBER: 28,003 REFERENCE/DOCKET NUMBER: FOWLKES=4C COMMUNICATION INFORMATION:
11958 222333747 222333747 222333747 222333747 2233377 2330 2330 2330 2330 2340 2440 2440 2440	cation US/09( cation US/09( TON):  FOWLKES, Dank FAY, Batian K FRELINGER, Jo HYDE DERUCSCI COM EQUENCES: 17 COM EQUENCES: 17 COM EQUENCES: 17 COM TONE CATION DATA ATION NUMBER DATE: 30-App TICATION: <00 TICATION TONE CATION DATA ATION NUMBER DATE: 31-MA TONE CATION NUMBER TONE CATION NU	DOCKET N
22222777777777777777777777777777777777	ALI  -827A-87  -0.61711  ALINFORMATION:  ALINFORMATION:  ALINFORMATION:  RAY, Brian K FRELINGER, Jeffrey HYDED-DENUSCHER, RO TITLE OF INVENTION:  NUMBER OF SEQUENCES: 178  CORPLESSED BROWDY AND NEI STREET: 624 NINTH Street CITY: Washington STATE: U.S.A.  CONTRY: U.S.A.  ZIP: 20001  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatib OPERATING SYSTEM: PC-DOS, SOFTWARE: Patentin Releas CURRENT APPLICATION DATA: APPLICATION NUMBER: US 09 FILING DATE: 30-Apr-1998 FILING DATE: 31-OCT-1997 APPLICATION NUMBER: PCT/U FILING DATE: 31-OCT-1997 APPLICATION NUMBER: PCT/U FILING DATE: 31-OCT-1997 APPLICATION NUMBER: US 08 FILING DATE: 10-OCT-1997 APPLICATION NUMBER: US 08 FILING DATE: 31-OCT-1997 APPLICATION NUMBER: US 08 APPLICATION NUMB	REGISIKATION NUMBER: 20,0  REFERENCE/DOCKET NUMBER: TELECOMMUNICATION: 10001 6100
	RESULT 1  US-09-069-827A-87  Sequence 87, Application US/09069827A  Sequence 87, Application US/09069827A  PATION: PATION: PRELINGER, Dana M FRELINGER, Jeffrey, HYDE-DERUYSCHER, ROJ HYDE-DERUYSCHER, ROJ TITLE OF INVENTION: IDENTIFICATION: NUMBER OF SEQUENCES: 178  COMPLESS: ADDRESSE: BROWDY AND NEIL STREET: 624 Ninth Street INFERENCE DECOUNTRY: U.S.A. ZIP: 20001  COMPUTER, U.S.A. ZIP: 20001  COMPUTER, IBM PC COMPATION MEDIUM TYPE: Floppy disk COMPUTER: 1BM PC COMPATION SOFTWARE: PATENTIN Releas CURRENT APPLICATION NUMBER: US/09 FILING DATE: 31-OCT-1996 APPLICATION NUMBER: PCT/UN FILING DATE: 31-OCT-1997 APPLICATION NUMBER: PCT/UN FILING DATE: 31-OCT-1996 ATTORNEY/AGENT INFORMATION: NUMBER: US OF PROPER STREET STRE	TELECOL
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NAME/KEY: misc feature
OTHER INFORMATION: GenBank ID No. 6566066: g2346968
PUBLICATION INFORMATION:
US-09-610-906-12
                                                                                                                            Sequence 10, Application US/09502653
Patent No. 6331426
GENERAL INFORMATION:
APPLICANT: Clausen, Ib Groth
APPLICANT: Schlein, Martin
APPLICANT: Schlein, Martin
APPLICANT: Schlein, Martin
APPLICANT: Bech, Lisbeth
APPLICANT: Bech, Lisbeth
APPLICANT: Bech, Lisbeth
APPLICANT: Strongard, Peter Rahbek
APPLICATION NUMBER: US/09/502,653
CURRENT FILING DATE: 1999-02-11
EARLIER APPLICATION NUMBER: PA 1999 00799
EARLIER FILING DATE: 1999-06-07
EARLIER FILING DATE: 1999-03-24
EARLIER FILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 52
SEARLIER FILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 52
LENGTH: 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/09610906
Patent No. 656606
GENERAL INFORMATION:
APPLICANT: Walker, Michael G.
APPLICANT: Volkmuth, Wayne
TILE BOF INVENTION: AQUADENN-8 VARIANT
FILE REFERENCE: PC-0012 CIP
CURRENT FILING DATE: 2000-07-06
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS:
SOFTWARE: PERL PROGram
SSOFTWARE: PERL PROGram
SSOFTWARE: PERL PROGram
SSOFTWARE: PERL PROGram
SSOFTWARE: PERL PROGram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Bacillus circulans
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ORGANISM: Rattus norvegicus
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Best Local Similarity 50.0°
Matches 4; Conservative
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Best Local Similarity 50.0
Matches 4; Conservative
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210 GYWEPAWI 217
43 GYWVINWQ 50
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                                                                                                                    US-09-502-653-10
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APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DUFFIN, DAVID J.
APPLICANT: BIPLANI, SUNILA
APPLICANT: BIPLANI, SUNILA
APPLICANT: BIPLANI, SUNILA
APPLICANT: BERRILL, BARBARA MCEOWEN
APPLICANT: SCHATZ, PETER JOSEPH
TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
TITLE OF INVENTION: USES
FILE REFERENCE: 0300-0014
CURRENT APPLICATION NUMBER: US/09/620,091
CURRENT PILLING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 491
SEQ ID NO 81
LENGTH: 16
TYPE: PRT
CREMENTSM: Attificial Sequence
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                                              ; Score 39; DB 4; Length 11;
Pred. No. 24;
4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                 Sequence 81, Application US/09620091
Patent No. 6716811
GENERAL INFORMATION:
APPLICANT: CWIRLA, STEVEN E.
APPLICANT: BALU, PALANI
                                              100.08;
                                                                      50.0%;
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ORGANISM: Proteus mirabilis
                                                                                          4; Conservative
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1 GYWWPDWG 8
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1 GYWCDPWT 8
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Best Local Similarity
Matches 4; Conserv
                                              Query Match
Best Local Similarity
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US-09-543-681A-7620
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US-09-620-091-81
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; Sequence 26841, Application US/09252991A; Sequence 26841, Application US/09252991A; Sequence 26841, Application US/09252991A; Sequence 26841, Application US/09252991A; Patent No. 2681705; GENERAL INFORMATION:
; APPLICATION: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS; FILE REPERRNCE: 10999-02-18; FRIOR PEDICATION NUMBER: US 60/074,788; FRIOR FILING DATE: 1998-02-18; PRIOR FILING DATE: 1998-07-27; NUMBER OF SEQ ID NOS: 33142; SEQ ID NO 26841
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                          APPLICANT: ADDOLL DESCRICT.
APPLICANT: MUKETJi, Pradip
APPLICANT: Mukerji, Pradip
APPLICANT: Huang, Yung-Shang
APPLICANT: Huang, Yung-Shang
APPLICANT: Huang, Yung-Shang
APPLICANT: Huang, Yung-Shang
APPLICANT: Pereira, Suzette L.
TITLE REFERENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR APPLICATION NUMBER: US 09/199.095
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-09-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 278
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GENERAL INFORMATION:
APPLICAN MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AM
TITLE OF INVENTION: ABRUGINOSA FOR DIAG
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US-09-252-991A-26841
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Best Local Similarity 50.0%; Ratches 4; Conservative 4;
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
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Best Local Similarity 50.0
Matches 4; Conservative
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108 GYWIFLWV 115
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261 GYWGGYWG 268
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US-09-252-991A-32031
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
GURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR PILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
ROMBER OF SEQ ID NOS: 28208
SEQ ID NO 15791
LENGTH: 274
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100.0%; Score 39; DB 4;
Best Local Similarity 50.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0
                                                                                                                                                                                                                        ; Sequence 15791, Application US/09248796A; Patent No. 6747137
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Patent No. 6403349
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
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; Sequence 18, Application US/09903456
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US-09-248-796A-15791
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Best Local Similarity 50...
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108 GYWIFLWV 115
                                       224 GYWDFHWI 231
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84 GYWPITWK 91
GYWXXXWX 8
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US-09-248-796A-15791
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US-08-415-751-6
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COUNTRY: United States of America
CONPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRYPTOSPORIDIUM ANTIBODIES, DNA AND RNA BROODING THEM, HYBRID VECTOR AND TRANSFORMED HOST AND METHODS FOR IMMUNOTHERAPY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLYPEPTIDES BINDING ANTI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1: PHILLIPS, MOORE, LEMPIO & FINLEY 385 Sherman Avenue, Suite 6
; FILE REFERENCE: 107196.136
CURRENT APPLICATION WUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              480.19-2 (HHD)
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SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,751
FILING DATE: 03-APR-1995
CLASSIFICATION: 435
FRIOR APPLICATION NUMBER: 08/071,880
FILING DATE: June 1,1993
APPLICATION NUMBER: 07/891,301
FILING DATE: May 29, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIAGNOSIS AND KIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08415751
Patent No. 5643772
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: NEECH, JAMES
APPLICANT: NEECH, JAMES
TITLE OF INVENTION: REPREPTIDES B
TITLE OF INVENTION: CRYPTOSPORIDIU
TITLE OF INVENTION: AND RAM ENCODI
TITLE OF INVENTION: AND RAM ENCODI
TITLE OF INVENTION: WECTOR AND TRA
TITLE OF INVENTION: DIAGROSIS AND
TITLE OF INVENTION: DIAGROSIS AND
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REGIETRATION NUMBER: 36,518
REFRENCE/DOCKET NUMBER: 480.
TELECOMMUNICATION INFORMATION:
TELEFAN: (415) 324-1677
INPORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                     ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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315 GYWRGPWR 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                       1 GYWXXXWX 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
STREET: 38
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US-08-415-751-6
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Second Solution Decided Solution Second Seco
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US-09-107-532A-6868
US-09-107-532A-6868
Sequence 6868, Application US/09107532A
Setent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION:
TITLE OF TIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 362;
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                                                                                                                                                                                                                                    Positions coded by nonsense codons are identified as Xaa.
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 39; DB 1;
Pred. No. 6.2e+02;
4; Mismatches 0;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILLING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: <Unknown>
MOLECULE TYPE: peptide ORIGINAL SOURCE: ORGANISM: Cryptosporidium parvum
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50.0%; P
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STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.v*
--- 4; Conservative
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Matches 4; Conservative
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276 GYWLVDWE 283
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NAME/KEY:
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LENGTH: 492 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23328
                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0
Matches 4; Conservative
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Best Local Similarity 50.0
Matches 4; Conservative
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111 GYWISAWL 118
                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                   1 GYWXXXWX 8
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                                                                                                                                     FEATURE
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Patent No. 6583275
GENBRAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                   NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REPERENCE/DOCKET NUMBER: GTC-012
RELECHMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEPRAX: (781)893-5007
INFORMATION POR SEQ ID NO: 6868:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 FILING TATION NUMBER: 60/051571 FILING DATE: July 2, 1997
APPLICATION NUMBER: 60/085,598
                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Enterococcus faecium
                FILING DATE: 14 May 1998
APPLICATION UNDRER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                   LENGTH: 478 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (781)893-8277
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SEQUENCE CHARACTERISTICS:
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STATE: Massachusetts
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Best Local Similarity 50.0°
....has 4; Conservative
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98 GYWLSAWL 105
                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
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US-09-107-532A-6945
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Sequence 23328

Sequence 23328

Sequence 23328

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: AUGUSIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 23328

LENGTH: 499
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                                                                                                                                                                                            Length 492;
                                                                                                                                                                                      100.0%; Score 39; DB 4; Length 49
50.0%; Pred. No. 8.2e+02;
tive 4; Mismatches 0; Indels
                                    , NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...492
; SEQUENCE DESCRIPTION: SEQ ID NO: 6945:
US-09-107-532A-6945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: January 3, 2005, 16:33:49 Job time: 23.04 sec8
ORGANISM: Enterococcus faecium
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19264, A 1, Appli 5, Appli 9, Appli

Sequence Sequence Sequence Sequence Sequence

Sequence 362818, Sequence 176036, Sequence 273234, Sequence 19269, Sequence 19264,

Sequence 173556, Sequence 260243, Sequence 357518, Sequence 86, Appl

Sequence ( Sequence ( Sequence (

Sequence

Sequence

US-10-425-115-324628 US-10-425-115-362818 US-10-425-126314 US-10-425-135-27324 US-10-362-493-19264 US-09-910-483-15 US-09-910-483-15 US-09-910-483-17 US-09-910-483-17 US-09-910-483-17 US-09-910-483-17 US-09-910-483-17 US-09-910-483-17 US-09-910-483-17 US-09-910-483-17 US-09-910-483-14 US-10-425-115-357518 US-10-425-115-3778 US-10-282-122A-68730 US-10-160-223-08 US-10-160-223-08

68730, A 54778, A 64112, A

Sequence Sequence

Sequence

Sequence

Sequence

184877

Sequence

Sequence Sequence :

US-10-282-122A-64263 US-10-425-115-344695 US-10-424-599-267810

US-10-424-599-184877

ALIGNMENTS

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Sequence 68, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGETA
; FILE REFERENCE: 28967/37084A
; CURRENT FILING DATE: 2002-01-15
; UNMBER OF SEQ ID NOS: 80
; SOFTWARE: PATENTIN vergion 3.0
; SEQ ID NO 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 39; DB 13;
Similarity 100.0%; Pred. No. 1.5e+06;
8; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Peptide
FEATURE:
NAME/KEY: SITE
LOCATION: (4)..(6)
COTHER INFORMATION: X is any amino acid
LOCATION: (8)..(8)
COTHER INFORMATION: X is any amino acid
US-10-046-922-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserv
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US-10-046-922-68
 LENGTH: 8
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Sequence 35, Appl
Sequence 73, Appl
Sequence 297, App
Sequence 476, App
Sequence 416, App
Sequence 31127, A
Sequence 287762,
Sequence 287762,
Sequence 170197,
                                                                                         January 3, 2005, 16:32:45; Search time 80.64 Seconds (without alignments) 35.687 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.ppp:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-425-115-287762
US-10-437-963-170197
US-10-425-115-308836
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US-10-046-922-36
US-10-046-922-34
US-10-046-922-73
US-10-046-922-73
US-10-462-262-297
US-10-260-066-476
US-09-864-761-35127
US-09-864-761-35127
                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                    1599051 seqs, 359727711 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                               Published_Applications_AA:*
                                                                  - protein search, using sw model
                                                                                                                                                                                                         BLOSUM62DX—'
Gapop 10.0', Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                                                  US-10-046-922-68
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Match Length
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                                                                  OM protein
                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                             Run on:
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Indels Length

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TYPE: PRT
ORGANISM: peptide library
FEATURE:
NAME/KEY: SITE
LOCATION: (5)..(7)
OTHER INFORMATION: X is any amino acid
LOCATION: (9)..(9)
OTHER INFORMATION: X is any amino acid
                                                                                                                                                                                        100.0%;
                                                                                                                                                                         TYPE: PRT; ORGANISM: isolated peptide US-10-046-922-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
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2 GYWLTIWG 9
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Best Local Similarity
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US-10-125-869A-73
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     Sequence 36, Application US/10046922
| Sequence 36, Application No. US20020164667A1
| GENERAL INFORMATION:
| APPLICANT: Alitalo, Kari
| APPLICANT: Koivunen, Erkki
| APPLICANT: Kubo, Hajime
| TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS FILE REFERENCE: 28967/37084A
| CURRENT APPLICATION NOWBER: US/10/046,922
| CURRENT FILING DATE: 2002-01-15
| NUMBER OF SEQ ID NOS: 80
| SOFTWARE: Patentin version 3.0
| SEQ ID NO 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-046-922-34
; Sequence 34, Application US/10046922
; Publication No. US2020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Koivunen, Erkki
; APPLICANT: Koivunen, Erkki
; TILE OF INVENTION: VGGRE-3 INHIBITOR MATERIALS AND METHODS
; FILE REPERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT PILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 39; DB 13; Length 10; 50.0%; Pred. No. 1.3e+02;
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50.0%; Pred. No. 1.5e+06;
tive 4; Mismatches 0;
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LOCATION: (1)..(1)
OTHER INFORMATION: X is any amino acid
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; OTHER INFORMATION: X is any amino acid US-10-046-922-34
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US-10-046-922-35
US-10-046-922-35
Sublication No. US20020164667A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Roivunen, Erkki
APPLICANT: Koivunen, Erkki
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Best Local Similarity 50.0'
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2 GYWLTIWG 9
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2 GYWWDTWF 9
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Best Local Similarity
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US-10-046-922-36
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LOCATION: (10)
US-10-046-922-36
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LENGTH: 10
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Gaps
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US-10-046-922-73
Sequence 73, Application US/10046922
Sequence 73, Application US/10046922
SHUDIcation No. US20020164667A1
GENERAL INFORMATION:
APPLICANT: Altalo, Kari
APPLICANT: Kubo, Hajime
TITLE OF INVERTION: VEGET 3 INHIBITOR MATERIALS AND METHODS
FILE REPERENCE: 28967/37084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT PILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 73
FEWANT: 12
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TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS FILE REFERENCE: 28967/37084A
CURRENT APPLICATION UNMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 35
LENGTH: 10
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Publication No. US20030199671A1

GENERAL INFORMATION:

APPLICANT: Wu, Qi-Long

APPLICANT: Wu, Qi-Long

APPLICANT: Ransohoff, Thomas C.

APPLICANT: Ransohoff, Thomas C.

APPLICANT: Potter, M. Daniel (deceased)

TITLE OF INVENTION: POLYPEPTIDES

TITLE OF INVENTION: POLYPEPTIDES

TITLE OF INVENTION: POLYPEPTIDES

TITLE OF INVENTION: US/10/125,869A

CURRENT APPLICATION NUMBER: US/10/125,869A
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100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0;
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Pred. No. 1.3e+02;
4; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
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SEQ ID NO 35127
LENGTH: 29
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/336,369
PRIOR PILING DATE: 2000-00-3
PRIOR PILING DATE: 2000-00-3
PRIOR PILING DATE: 2000-00-4
PRIOR PILING DATE: 2000-00-7
PRIOR PILING DATE: 2000-00-7
PRIOR PILING DATE: 2001-01-30
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PRIOR PLING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-31
PRIOR PLING DATE: 2000-09-31
PRIOR PLING DATE: 2000-09-31
PRIOR PLING DATE: 2000-09-30
PRIOR PLING DATE: 2000-09-30
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PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 35127, Application US/09864761 Patent No. US20020048763A1
                            ; LENGTH: 25; TYPE: PRT ORGANISM: Eschericia coli PEATURE: NAME/KBY: MISC FEATURE; NAME/KBY: MISC FEATURE; OTHER INFORMATION: Tiel-20C-3-D116
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6 GYWGELWG 13
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        SEQ ID NO 476
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APPLICANT: Pissette, Renee
APPLICANT: Brissette, Renee
APPLICANT: Brissette, Renee
APPLICANT: Brissette, Renee
APPLICANT: Blume, Arthur J.
APPLICANT: Blume, Arthur J.
APPLICANT: Goldstein, Neil I.
TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USB FOR IDENTIFYING TARGET BINE FILE REPERBENCE: 2598-4009091.
CURRENT APPLICATION UNMBER: US/10/280,066
CURRENT FILING DATE: 2002-10-24
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                                                                                                                                                                                                                                                                                                                                        Length 13;
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                                                                                                                                                                                                                                                                                                                                100.0%; Score 39; DB 14;
50.0%; Pred. No. 1.6e+02;
tive 4; Mismatches 0;
                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Pc region binding polypeptide
US-10-125-869A-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-462-262-297
US-10-462-262-297
Sequence 297, Application US/10462262
PUDLication No. US20040009534A1
GENERAL INFORMATION:
APPLICANT: Satc, Aaron K.
APPLICANT: Dawson, Bruce M.
TITLE OF INVENTION: PROTEIN ANALYSIS
FILE REFERENCE: 10280-052001
CURRENT APPLICATION NUMBER: US 60/388,642
FRIOR APPLICATION NUMBER: US 60/388,642
PRIOR APPLICATION NUMBER: US 60/388,642
PRIOR APPLICATION NUMBER: US 60/388,642
PRIOR APPLICATION NUMBER: US 60/388,642
SPRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 430
SOFTWARE: FastEEQ for Windows Version 4.0
PRIOR APPLICATION NUMBER: 60/284,534
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 200
SEQ ID NO 73
LENGTH: 13
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PRIOR FILING DATE: 2001-10-24
                                                                                                                                                                                             ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1
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Best Local Similarity 50.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         GYWXXXWX 8
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GYWCNVWG 8
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                       TYPE: PRT
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APPLICANT: Barbauk, Brad
APPLICANT: Li, Plan
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 287762, Application US/10425115
Sequence 287762, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
CAPPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 30-216322)B
FURRENT APPLICATION WUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 287762
LENGTH: 47
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                                                                                OTHER INFORMATION: MAP TO AC009503.3

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
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US-10-425-115-287762
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50.0%; Pred. No. 4.6e+02;
iive 4; Mismatches 0;
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50.0%; Pred. No. 3.6e+02;
tive 4; Mismatches 0
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La ROSa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0
Matches 4; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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25 GYWQLHWM 32
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Best Local Similarity
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ORGANISM: Zea mays
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                                                          FEATURE:
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Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
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                                FEATURE:
OTHER INFORMATION: MAP TO AC009503.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.97
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.94
OTHER INFORMATION: EXPRESSED IN BEAIN, SIGNAL = 0.91
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.91
OTHER INFORMATION: EST_HUMAN HIT: AA343827.1, EVALUE 1.80e+00
                                                                                                                                                                                                                                                                                                           100.0%; Score 39; DB 9; Length 29;
S0.0%; Pred. No. 3.10+02;
iive 4; Mismatches 0; Indels
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CURRENT PAPLICATION NUMBER: US/09/864,761
CURRENT PILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-08-36
PRIOR PELING DATE: 2000-08-36
PRIOR PELING DATE: 2000-09-37
PRIOR APPLICATION NUMBER: US 60/23,36
PRIOR PELING DATE: 2000-09-37
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PELING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-30
PRIOR PILING DATE: 2000-09-30
PRIOR FILING DATE: 2000-09-30
PRIOR PILING DATE: 2
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      ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-864-761-35127
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US-09-864-761-40409
                                                                                                                                                                                                                                                                                                                                                                            Matches
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Search completed: January 3, 2005, 16:54:15 Job time: 81.64 sec8
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Best Local Similarity 50.04
Matches 4; Conservative
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41 GYWQKQWL 48
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7 GYWTPFWL 14
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US-10-425-115-362818
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Sequence 308836, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Acvalic, David K.
APPLICANT: Applicant Rovalic, David K.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 308836
LENGTH: 58
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US-10-425-115-324628

Sequence 324628, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yahua
APPLICANT: Cab, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFRENCE: 38-21 (53222)
CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 324628

LENGTH: 61
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CTHER INFORMATION: Clone ID: PAT_MRT4530_68546C.1.pep US-10-437-963-170197
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                                                                                                                                                                               Query Match
100.0%; Score 39; DB 16;
Best Local Similarity 50.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 4; Mismatches 0;
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US-10-425-115-308836
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NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 170197
LENGTH: 57
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Best Local Similarity 50.0°
Matches 4; Conservative
                                                             TYPE: PRT
ORGANISM: Oryza sativa
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19 GYWLFMWV 26
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49 GYWGASWN 56
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ORGANISM: Zea mays
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Sequence 362818, Application US/10425115
Sequence 362818, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 362818
LENGTH: 62
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; Score 39; DB 17; Length 61;
Pred. No. 5.7e+02;
4; Mismatches 0; Indels
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50.0%; Pred. No. 5.8e+02;
tive 4; Mismatches 0; Indels
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US-10-425-115-362818
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ORGANISM: Zea mays
PEATURE:
NAME/KEX: unsure
LOCATION: (1)..(62)
OTHER INFORMATION: unsure at all Xaa locations
Query Match
Best Local Similarity 50.0%;
Matches 4; Conservative 4
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 3, 2005, 16:20:13; Search time 17.92 Seconds (without alignments) 42.954 Million cell updates/sec

US-10-046-922-68 39 1 GYWXXXWX 8 score: Sequence: Perfect

Scoring table:

BLOSUM62DX: Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES	ripti	lysis protein S -	etical p				hypothetical prote		hypothetical prote	CDPdiacylglycerol-	hypothetical prote	arginine-tRNA-prot	probable mccF prot		aquaporin 8 - rat	phosphatidate cyti		probable ABC trans	hypothetical prote	probable sugar ABC	protein F41H10.7 [	oligopeptide ABC t	hypothetical prote	_				F	siderophore/Surfac	conserved hypothet
SUMMARIES	ΙD	S22905	T03190	E69903	S12193	C34903	G83047	S76385	D87264	873905	A69843	F82733	E75325	JC5806	JC5622	F83188	JC4832	E95268	AB2307	H95869	E88690	G72215	C83886	C82611	T37139	AE2047	D82500	C95307	7	AB0301
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de	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0			100.0	100.0	100.0	100.0	100.0	100.0
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466 2 T35164 472 2 E83497 475 2 E83497 482 2 J46116 490 2 C86879 508 2 C9588 517 2 A11201 519 2 S7772 519 2 S7772 519 2 C9588 514 2 T15414 535 2 B95552 535 2 G95339 541 2 AC2392 541 2 AC2392	probable secreted ABC transporter (a	probable amino aci arginine/ornithine arginine/ornithine	arginine/ornitine arginine/ornitine	probable ABC trans hypothetical prote	oligopeptide trans probable carbohydr	hypothetical prote probable dipeptide	probable ABC trans	
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	T35164 D70048	E83497 T46745 JH0110	C86879 G86878	C95282 AI3201	S77572 E83268	T15414 B95952	G95389	AH2975
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# ALIGNMENTS

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                         C;Species: phage 21
C;Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 08-Oct-1999
C;Accession: S22905
                                                                                                                                                                                                                                                                                                                                                   A.Gene: S.

C.Keywords: alternative initiators; cell wall lysis; transmembrane protein E;1-71/Product: lysis protein inhibitor S107 #status predicted <MATI>
E;1-71/Product: lysis protein S105 #status predicted <MATI>
E;7-28/Domain: transmembrane #status predicted <TMI>
E;7-28/Domain: transmembrane #status predicted <TMI>
                                                                                                                                                                                                                 A,Accession: S22905
A,Molecule type: DNA
A,Rosidues: 1-71 <BON>
A,Cross-references: EMBL:M65239; NID:g215466; PIDN:AAA32349.1; PID:g215467
C,Genetics:
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                                                                                                        R;Bonovich, M.T.; Young, R.
J. Bacteriol. 173, 2897-2905, 1991
A;Tille: Dual start mocif in two lambdoid S genes unrelated to lambda A;Reference number: S22905; MUID:91210180; PMID:2019562
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Best Local Similarity 50.0
Matches 4; Conservative
lysis protein S - phage 21
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|||:::|: 21 GYWFLQWL 28 원

hypothetical protein 72B - rice mitochondrion
CjSpecies: mitochondrion Oryza sativa (rice)
CjDate: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
CjAccesion: T03190
R;Itadani, H.; Wakasugi, T.; Sugita, M.; Sugiura, M.; Nakazono, M.; Hirai, A.
Plant Cell Physiol. 35, 1239-1244, 1994
A;Title: Nucleotide sequence of a 28-Kpp portion of rice mitochondrial DNA: the existence A;Reference number: Z14841; MUID:95211382; PMID:7545979
A;Accession: T03190
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: DNA
A;Residues: 1-72 - ITA>
A;Cross-references: UNIPROT:Q35302; EMBL:D32052; NID:g769704; PIDN:BAA06811.1; PID:g7697(C;Genetics:

A;Genome: mitochondrion C;Keywords: mitochondrion

100.0%; Score 39;

Length 72;

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Query Match

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A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76385
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126 GYWFAYWG 133
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                              RESULT 3
B69903
hypochetical protein yodi - Bacillus subtilis
C;Species: Bacillus subtilis
C;Accession: E69903
R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M; Alloni, G; Azevedo, V; Berrer
C; Broni, S.D; Emmerson, P.T; Entian, K.D.; Errington, J; Fabret, C; Ferrari, E. Nature 300, 249-256, 1997
N; Hundors: Foulger, D; Fritz, C; Fujita, M; Fujita, X; Fupare, C; Ferrari, E. Nature 300, 249-256, 1997
N; Hundors: Foulger, D; Fritz, C; Fujita, M; Kurite, X; Japhidus, A; Hullo, M; E. Noetter, P; Koningstein, G; Krooph, S; Kumano, M; Kurite, X; Japhidus, A; Janada, S; Maueell
Y; M; Ogawa, K; Ogiwara, A; Oudega, B; Rose, M; Sedaje, V; Sada, T; Naturell
R; Rieger, M; Rivolta, C; Rocha, E; Roche, M; Sodaje, Y; Sada, T; Naturell
A;Authors: Schleich, S; Schroeter, R; Scoffone, P; Sekiguchi, J; Sekowska, A; Serventin, A; Vannanoto, M; Tomato, M; Sekiguchi, J; Sekowska, A; Tranakoshi, A; Tanakoshi, A; Tanakoshi, A; Tanakoshi, A; Yannanoto, M; Yannanoto, M; Yannanoto, M; Tomato, M; Yannanoto, M; Yannano, M; Tomato, M; Yannano, M; A; Tanakoshi, A; Yannanoto, M; Yannano, M; A; Yannanoto, M; Yannano, M; A; Yannanoto, M; Yannano, M; A; Yannano, M; Yann
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$12193
hypothetical protein 4 - Thiobacillus ferrooxidans plasmid pTF1
c;Species: Thiobacillus ferrooxidans
c;Species: Thiobacillus ferrooxidans
c;Species: Thiobacillus ferrooxidans
c;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
c;Accession: $12193
R;Drodlet, M; Zanga, P; Lau, P.C.K.
Ribrodlet, M; Zanga, P; Lau, P; Lau
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C;Genetics:
A;Genome: plasmid pTF1
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    Pred. No. 51;
4; Mismatches
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50.0%;
                                              4; Conservative
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89 GYWRSSWR 96
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Best Local Similarity
Matches 4; Conserv
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C,Accession: C34903
R;Bedayk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1390
J,Tile: Active site structure and antigen binding properties of idiotypically cross-reactive number: A34903; MUD: 90094387; PMID:2104617
A;Reference number: A34903; MUD: 90094387; PMID:2104617
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: G83047
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Jory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogareference number: A62950; MUID:20437337; PMID:10984043
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A;Residues: 1-187 <STO>
A;Cross-references: UNIPROT:Q9HV15; GB:AE004892; GB:AE004091; NID:g9951049; PIDN:AAG0817:
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C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S76385
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
DNA Res. 3, 109-136, 1996
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Ig heavy chain precursor V region (5-27) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996
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C, Superfantly: immunoglobulin V region; immunoglobulin homology C, Steywords: hereroterramer; immunoglobulin P;34-119/Domain: immunoglobulin homology <IMM>
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C;Species: Bacillus subtiles subtiles controls subtiles subtiles controls subtiles subtiles subtiles subtiles subtiles subtiles c;Species: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004 C;Species: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004 C;Species: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004 C;Species: 05-Dec-1997 S; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chon A; Birlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, B. Natures 390, 249-256, 1997 M; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maauda, S.; Maneel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecelle, Rieger, M.; Rivolta, C.; Rocha, B.; Roose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schlach, S.; Schrocter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, T.; Minters, P.; Winter, P.; Voshida, K.; Yasan, K.; Yoshida, K.; Yata, K.; Yoshida, K.; A; Authors: Yoshikawa, H.F.; Zumstein, B.; Yoshikawa, H.; Danchin, A.; Hencomplete genome sequence of the Gram-positive bacterium Bacillus subtilis.
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A;Experimental source: strain 168
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C;Superfamily: Bacillus subtilis hypothetical protein yjbA
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50.0%; Pred. No. 1.6e+02;
tive 4; Mismatches 0;
                                                                                                                                                                                                                                        - Bacillus subtilis
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                                                                                                                                                                                                                                           hypothetical protein yjbA
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84 GYWARKWR 91
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Matches 4; Conserv
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C;Species Mycoplasma pneumoniae
A;Variaty: ATCC 29342
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
R;Himmelreich, R.;Hilbert, H.; Plagens, H.; Pirkl, B.; Li, B.C.; Herrmann, R. Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae A;Reference number: S7330; MUID:97105885; PMID:8948633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein CC0125 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: CaloApr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: D87246
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Luab, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 99, 4136-4141, 2001
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                       PIDN: BAA1023
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Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-218 <STO>
A;Cross-references: UNIPROT:Q9ABU5; GB:AE005673; NID:g13421234; PIDN:AAK22112.1; GSPDB:
C;Genetics:
A;Gene: CC0125
                                                                                                   EMBL:D64000; GB:AB001339; NID:g1001484; PIDN: submitted to the EMBL Data Library, June 1996
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                                                                                                                                                                                                                                100.0%; Score 39; DB 2; Length 218; 50.0%; Pred. No. 1.40+02; ive 4; Mismatches 0; Indels
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                            A,Molecule type: DNA
A,Residues: 1-218 «KAN»
A,Cross-references: UNIPROT.Q55705; EMBL:D64000; G
A,Note: the nucleotide sequence was submitted to t
C,Superfamily: probable alkaline phosphatase yngC
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4; Mismatches
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GYWRPAWR 146
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GYWVGRWG 81
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Best Local Similarity
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Matches 4; Conserv
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Status: preliminary
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Date: 09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: JCSSALA
R;Ishibashi, K.; Kuwahara, M.; Kageyama, Y.; Tohsaka, A.; Marumo, F.; Sasaki, S.
Biochem. Biophys. Res. Commun. 237, 714-718, 1997
A;Tille: Cloning and functional expression of a second new aquaporin abundantly expressec
A;Reference number: JCSS22; MUID:97445104; PMID:9299432
A;Contents: Testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: JC5622
A;Molecule type: mRNA
A;Residues: 1-263 <ISH>
A;Crost-references: UNIPROT:P56405; DDBJ:AB005547; NID:g2346967; PIDN:BAA21918.1; PID:g2:
C;Comment: This protein is a water channel protein which plays a role in the regulation c
C;Cuperfamily: lens fiber membrane major intrinsic protein
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F:231-250/Domain: transmembrane #status predicted <TM6>
F:141/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 100.0%; Score 39; DB 2; Length 26 Local Similarity 50.0%; Pred. No. 1.7e+02; Local 4; Conservative 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;109-130/Domain: transmembrane #status predicted <TM3>F;159-179/Domain: transmembrane #status predicted <TM4>F;182-204/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Keywords: glycoprotein
F;35-59/Domain: transmembrane #status predicted <TM1>
F;65-84/Domain: transmembrane #status predicted <TM2>
F;94-96/Region: NPA motif
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GYWDFHWI 229
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224 GYWDFHWI 231
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A;Molecule type: DNA
A;Residues: 1-271 <STO>
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                                                                                                                                                                                            aquaporin 8 - rat
                                                   222
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Best Local
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A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable mccF protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: E75325
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Status: preliminary
Modecule type: DNA
A,Readiques: 1-257 «WHL>
A,Cross-references: UNIPROT:Q9RSX1; GB:AE002038; GB:AE000513; NID:g6459790; PIDN:AAF1155
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C;Date: 27-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Date: 27-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Accession: JCS806
R;Ma, T: Yang, B:, Verkman, A.S.
Biochem. Biophys. Res. Commun. 240, 324-328, 1997
A;Title: Cloning of a novel water and urea-permeable aquaporin from mouse expressed strce. A;Reference number: JC5806; MUID:98049830; PMID:9388476
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A;Residues: 1-261 <MAA.
A;Cross-references: UNIPROT: P56404; DDBJ:AP018952; NID:g2353796; PIDN:AAB68847.1; PID:g2
C;Comment: This protein functions as a mercurial-sensitive water channel.
C;Superfamily: lens fiber membrane major intrinsic protein
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;92-94/Region: NPA motif
;210-212/Region: NPA motif
;85,139/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                        100.0%; Score 39; DB 2; Length 254; 50.0%; Pred. No. 1.6e+02; ive 4; Mismatches 0; Indels
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Best Local Similarity 50.09
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Best Local Similarity 50.0
Matches 4; Conservative
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22 GYWPDRWA 29
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Length 263;

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C;Accession: F83188
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Briadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc A;Reference number: A62950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q59640; GB:AE004785; GB:AE004091; NID:g9949809; PIDN:AAG07033:
A;Experimental source: strain PAO1
phosphatidate cytidylyltransferase PA3651 [imported] - Pseudomonas aeruginosa (strain PAC C,Species: Pseudomonas aeruginosa
C,Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
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50.0%; Pred. No. 1.7e+02;
iive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: phosphatidate cytidylyltransferase
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(without alignments)
47.317 Million cell updates/sec
                                                                                                                                                               January 3, 2005, 16:12:00 ; Search time 97.28 Seconds
GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                          OM protein - protein search, using sw model
                          Copyright
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Run on:

US-10-046-922-68 39 1 GYWXXXWX 8 Title: Perfect score: Sequence:

Scoring table: <u>ABLOSUM62DX</u>3 Gapop 10.0 , Gapext 0.5

1825181 Total number of hits satisfying chosen parameters:

1825181 segs, 575374646 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: uniprot_sprot:*
2: uniprot_trembl:* UniProt_02:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

-	Description	Q7udb7 shigella fl	Q9evpl escherichia						Q83s57 shigella fl					P20088 thiobacillu	Q728a6 desulfovibr	Aas97170 desulfovi	Q72d02 desulfovibr	Aas95609 desulfovi	Q7u7v6 synechococc				Q7tuv7 prochloroco	Q6nf17 corynebacte	_			Q7w0p5 bordetella			Q7wl18 bordetella	Q9ky37 streptomyce
SUMMAKIES	ID	Q7UDB7	Q9EVP1	VLYS BPP21	Q7C2 <u>3</u> 0	Q9FCW3	Q7UDP0	Q83ML2	Q83S57	Q35302	YODI_BACSU	Q95S05	Q611L4	YML2 THIFE	Q728 <u>A</u> 6	AAS97170	Q72D02	AAS95609	971170	Q8MK57	Q7U395	Q7VBG3	Q7TUV7	Q6NF17	CAE50615	Q9HV15	Q88QB8	Q7W0P5	Q7W3F9	Q7WES9	Q7WL18	Q9KY37
	ength DB	30 2	49 2	71 1	71 2	71 2	71 2	71 2	71 2	72 2	83 1	89 2	102 2	108 1	120 2	120 2	122 2	122 2		128 2	130 2		135 2					204 2	204 2	204 2	212 2	213 2
ď	Query Match Length	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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	Result No.	<u></u>	7	3	4	S	9	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

[1] SEQUENCE FROM N.A. STRAIN=H.I.8.;

Q8a8u4 bacteroides Q55705 synechocyst Q7vzm7 bordetella Q9abu5 caulobacter Q88486 zea mays (m P75520 mycoplasma Q72kr5 thermus the Aa880801 thermus the Aa880801 thermus the Q7wm10 bordetella Q9wgw9 human immun Q8gx61 arabidopsis Q31597 bacillus su O32816 lactococcus Q9pelo xylella fas	
QBABU4 1212_SYNY3 QYVZM7 QSABU5 QSABU5 QSABU6 QYSAB QYZYNQ QYWYNQ QYWYNQ QSWGW9 QBGX61 QSGX61 Q31159 Q31159 Q31154	
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2114 2218 2224 2228 2328 2335 243 253	
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ALIGNMENTS

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Gарв
                                                                                                                                             Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Shigella.
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Enterobacteriaceae, Escherichia.
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                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
STRAIN=24577.
STRAIN=24577,
Mei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Wei J., Goldberg M.B., Plunkett G. III, Rose D.J., Darling A
Mau B., Perna N. T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
Schwartz D.C., Blattner F.R.;
"Complete genome sequence and comparative genomics of Shigella
flexenci serotype 2a strain 2457T.";
Infect. Immun. 71:2775-2786 (2003).
EMBL; AE016980; AAP16193.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 39; DB 2; Length 30; 50.0%; Pred. No. 1.9e+02; ive 4; Mismatches 0; Indels
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
S protein (Fragment)
Escherichia coli.
                                                     01-007-2003 (TrEMBLrel. 25, Created)
01-007-2003 (TrEMBLrel. 25, Last sequence update)
01-0AR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical bacteriophage protein.
Name-ybcR, OrderedLocusNames=S0714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 AA.
                            30 AA.
                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007054; Lygis_S.
Pfam; PP04971; Lygis_S; 1.
Hypothetical protein.
SEQUENCE 30 AA; 3404 MW:
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                            PRELIMINARY;
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21 GYWFLQWL 28
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Best Local Similarity
Matches 4; Conserv
                                                                                                                               Shigella flexneri
                                                                                                                                                                                NCBI_TaxID=623;
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                            Q7UDB7
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Q9EVP1
RESULT 1
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Matches

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Schmidt H., Scheef J., Morabito S., Caprioli A., Wieler L., Karch H.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ270998; CAC05565.1; -

InterPro; IPR007054; Lysis S.

Pfam; PF04971; Lysis S; 1.

SEQUENCE 71 AA; 7923 MW; 984D68F25220B7E2 CRC64;
                                                                                                                                         MEDLINE=22590274; PubMed=12704152; MEDLINE=22590274; PubMed=12704152; Mei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Pournier G., Maylew G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.; Schwartz D.C., Blattner F.R.; Schwartz D.C., Blattner F.R.; Inferce genome sequence and comparative genomics of Shigella flaxneri serotype za strain 24577."; Infect. Immun. 71:2773-2786(2003).

EMBL; ABO16980; AAP16205.1; -..
EMBL; ABO16980; AAP16205.1; -..
Pfam; PF04971; Lysis S.
Pfam; PF04971; Lysis S.
Pfam; PF04971; Lysis S. 1.
ENGUENCE 71 AA; 7914 MW; 10CEIC485234AE99 CRC64;
               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unkmeir A., Schmidt H.;
"Structural analysis of phage-borne stx genes and their flanking sequences in shiga toxin-producing Escherichia coli and Shigella dysenteriae type 1 strains.";
Infect. Immun. 68:4856-4864(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 39; DB 2; Length 71; 50.0%; Pred. No. 4e+02; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 39; DB 2; Length 71;
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                          50.0%; Pred. No. 4e+02;
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MEDLINE=20407286; PubMed=10948097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterobacteriaceae; Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
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21 GYWFLQWL 28
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21 GYWFLQWL 28
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Best Local Similarity
Matches 4; Conserv
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Shigella flexneri
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                                                             NCBI_TaxID=623;
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                                                                                                                          STRAIN=2457T
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MEDLINE=91210180; PubMed=2019562;
MEDLINE=912.0180; PubMed=2019562;
MEDLINE=91210180; Young R.;
Boal start motif in two lambdoid S genes unrelated to lambda S.";
J. Bacteriol. 173:2897-2905(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriophage P21 (Bacteriophage 21).
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
               Unkmeir A., Schmidt H.;

"Structural analysis of phage-borne stx genes and their flanking sequences in shiga toxin-producing Escherichia coli and Shigella dysenteriae type 1 strains.";

Infect. Immun. 68:4856-4864(2000).

EMBL; AA271139; CAC05573.1;

InterPro; IPR00/D54; Lysis_S.

Pfam; PP04971; Lysis_S.

NON_TER.

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Pfam; PF04971; Lyais_S; 1.
Phage lysis protein.
SEQUENCE 71 AA; 7893 MW; 8690A8F25234A3E2 CRC64;
                                                                                                                                                                                                           49 AA; 5227 MW; 0B6914DD9AE25E00 CRC64;
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Last sequence update)
Last annotation update)
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01-AUG-1992 (Rel. 23, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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MEDLINE=20407286; PubMed=10948097;
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Q7C2JO;
09-JUL-2004 (TREMBLEE]. 27, C;
05-JUL-2004 (TREMBLEE]. 27, L;
05-JUL-2004 (TREMBLEE]. 27, L;
PLATATIVE S PYOTENIN.
OrderedLocusNames=S0731;
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es 4; Conservative
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Best Local Similarity 50.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
VLYS_BPP21
ID VLYS_BPP21
AC P273\overline{6}0;
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Gaps

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RESULT 4 Q7C2J0

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RESULT 6

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Yu J.;
"Genome sequence of Shigella flexneri 2a: insights into pathogenicity
"Genome sequence of Shigella flexneri 2a: insights into pathogenicity
through comparison with genomes of Escherichia coli K12 and O157.";
Nucleic Acids Res. 30:4432411;
EMBL; ABO15099; AAN42324.1;
InterPro; IPR007054; Lysis_S.
Pfam; PF04971; Lysis_S; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang E., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A, Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The rps3-rpl16-nad3-rps12 gene cluster in rice mitochondrial DNA is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitochondrion.
Mitochondrion.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Ory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacřeria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-95308541; PubMed=7788722;
Nakazono M., Itadani H., Wakasugi T., Tsutsumi N., Sugiura M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 39; DB 2; Length 71; 50.0%; Pred. No. 4e+02;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
ORF72B.
                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                         71 AA
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                                                                                                                                                                                                                                                                                                                                   Created)
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24,
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                                                                                                                                                                                                                                                         PRELIMINARY;
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                                      [||:::|:
21 GYWFLQWL 28
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21 GYWFLQWL 28
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Best Local Similarity
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Matches
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MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22590274; PubMed=12704152; Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Dang W., Pournier G., Mayhew G.P., Plunkett G. III, Rose D.J., Darling A., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.;
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Enterobacteriaceae, Shigella.
                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T."; Infect. Immun. 71:2775-2786(2003).
EMBL, AED16979, AAP15795-1; -. Interpro; IPR07054; Lysis_S. Pfam; PF04971; Lysis_S. Pfam; PF04971; Lysis_S: 1. SEQUENCE 71 AA; 7881 MW; AB82BAF25234BC15 CRC64;
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SEQUENCE 71 AA; 7865 MW; AB90A8F25234A3F5 CRC64;
                                                                                                                                                                                   Last sequence update)
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Matches 4; Conservative
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21 GYWFLQWL 28
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Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

A Azevedo V., Betrero M.G., Bessieres P., Bolotin A., Borchert S.,

Borriss R., Boursier L., Brausn A., Braun M., Brignell S.C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Benizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

Benizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

Benizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

A Ghim S.V., Glaser P., Golfeuu A., Golightly S.J., Grandi G.,

Ghim S.V., Glaser P., Goffeuu A., Golightly S.J., Grandi G.,

A Guiseppi G., Guy B.J., Hage K., Haiech J., Harwood C.R., Henaut A.,

Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,

A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,

A Klein C., Kobayashi Y., Koetnet D., Kasahara Y., Kroningstein G., Krogh S.,

Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,

A Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,

A Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,

Noback M., Noone D., O'Really M., Ogawa K., Ogiwara A., Oudega B.,

Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ghim S.-Y., Jeong Y.-M., Choi S.-K., Park S.-H.; "Sequence analysis of the 30 kb region (182') of the Bacillus subtilis chromosome containing the cge cluster."; Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Wedler H., Lapidus A., Sorokin A., Ehrlich S.D.; Wambutt R., Wedler H., Lapidus A., Sorokin A., Ehrlich S.D.; Sequence analysis of the Bacillus subtilis chromosome region between the odhaB and sspC loci cloned in a yeast artificial chromosome."; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                               MEDLINE=95211382; PubMed=7545979;
Itadani H., Wakasugi T., Sugita M., Sugiura M., Nakazono M., Hirai A "Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA: "Nucleotide sequence of a 28-kbp portion of rice mitochondrial the existence of many sequences that correspond to parts of mitochondrial genes in intergenic regions.";
Plant Cell Physiol. 35:1239-1244(1994).

EMBL; D32052; BAA06811.1; -.

GO; GC; GO; GO; C; Mitochondrion; IEA.
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2004 (Rel. 45, Last annotation update)
Hypothetical protein yodi.
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transcribed from alternative promoters.";
Curr. Genet. 27:184-189(1995).
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                                                                             SEQUENCE FROM N.A.
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YODI_BACSU
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Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaler Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffene F., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Vári A., Wambutt R., Wedler E., Wedler F., Weltzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A., The Complete genome sequence of the Gram-positive bacterium Bacillus
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 89;
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50.0%; Pred. No. 4.9e+02;
ive 4; Mismatches 0; Indels
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PIR, E69903; E69903.
Subtlist; BG13537; yodl.
InterPro; IPR008991; Transl SH3_like.
Complete proteome; Hypothetical protein; Transmembrane.
TRANSMEM
58
SEQUENCE 83 AA; 9194 MW; 99FSBEA2F0F36A43 CRC64;
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Last annotation update)
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Best Local Similarity 50.vv
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Best Local Similarity 50.v.
L.a 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 390:249-256(1997).
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RESULT 12

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PubMed=15077118; DOI=10.1038/nbt959; PubMed=15077118; DOI=10.1038/nbt959; PubMed=15077118; DOI=10.1038/nbt959; PubMed=15077118; DOI=10.1038/nbt959; PubMed=15077118; DOI=10.1038/nbt959; PubMed=150.7, Eisen T.A., Faveman S.A., Methe B.A., Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R., Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J., Dieterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D., Dieterson J.D., Davidsen T.M., Khouri H.M., Gill J., Utterback T.R., Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.; Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.; Desulfevibrio vulgaris Hildenborough."; Pubmed Sequence of the anaerobic, sulfate-reducing bacterium Desulfevibrio vulgaris Hildenborough.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=15077118; Haveman S.A., Hemme C.L., Paulsen I.T., Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T., Kolonay J.F., Eisen J.A., Ward N., Methe B.A., Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R., Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
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Desulfovibrionaceae; Desulfovibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio.
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                                                Length 108;
                                                                                                      0; Indels
108 AA; 12335 MW; A8E67717C109A57E CRC64;
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SEQUENCE 120 AA; 13418 MW; CD3581657D76E183 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Lipoprotein, putative.
OrderedLocusNames=DVU2698;
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Last sequence update)
Last annotation update)
                                                   100.0%; Score 39; DB 1;
50.0%; Pred. No. 5.8e+02;
iive 4; Mismatches 0;
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4; Mismatches
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                                                                                                      4; Conservative
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DVU2698.
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89 GYWRSSWR 96
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                                                                     Local Similarity
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Matches 4; Conserv
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                                                                                                                                                      1 GYWXXXWX
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26-APR-2004 (
26-APR-2004 (
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AAS97170
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Drolet M., Zanga P., Lau P.C.K.;
"The mobilization and origin of transfer regions of a Thiobacillus ferrocxidans plasmid: relatedness to plasmids RSF1010 and pSC101.";
Mol. Microbiol. 4:1381-1391(1990).
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NCBI_TaxID=920,
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                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

NCBI_TaxID=7227,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 39; DB 2; Length 102; Pred. No. 5.5e+02; 4; Mismatches 0; Indels
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01-FEB-1991 (Rel. 17, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical 12.3 kDa protein in mobl 3'region (ORF 4).
Thiobacillus ferrooxidans.
                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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50.0%; P
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Hypothetical protein; Plasmid
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70 GYWQCNWE 77
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73 GYWIQEWS 80
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                                                                                                                                                                                                                                                                                                             ORFNames=HDC17696;
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Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D.,
Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
"The genome sequence of the macrobic, sulfate-reducing bacterium
Desulfovibrio vulgaris Hildenborough.";
Nat. Biotechnol. 22:554-559(2004).
BMBL, AE017318; AAS97170.1; -.
TICR: DVUZ698; -.
Lipoprotein.
SEQUENCE 120 AA; 13418 MW; CD3581657D76E183 CRC64;
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100.0%; Score 39; DB 2; Length 120;
Best Local Similarity 50.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 4; Mismatches 0; Indels
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Search completed: January 3, 2005, 16:32:33 Job time : 97.28 secs

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January 3, 2005, 17:22:59 ; Search time 154 Seconds (without alignments) 18.635 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                             BLOSUM62DX 4
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                   US-10-046-922-68
39
1 GYWXXXWX 8
                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum_DBsseq@length: 18___
                                                                                                                                                                                     Title:
Perfect score:
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                                                                                                             Run on:
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Post-processing: Minimum Match 0# Maximum Match 100# Listing first 45 summaries Listing first 45 summaries A.Geneseq23Sep04:* 1: geneseqp1980s:* 2: geneseqp200s:* 4: geneseqp2001s:* 5: geneseqp2001s:* 6: geneseqp2001s:* 7: geneseqp2001s:* 8: geneseqp2001s:* 7: geneseqp2001s:* 8: geneseqp2001s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Abp53965 VEGFR-3 b	Aay76794 Somatosta	Abp53964 VEGFR-3 b	Abp53418 Backbone	Adj25834 Tyrosine	_	Abp24270 HIV A24 m	HIV	Abp15892 HIV A24 8		m		Aar08140 Neurokini	Aay76792 Somatosta	_	Aap61465 Cyclic oc	Aap90981 Water-ins	Aar14237 Somatosta	Aar15362 Somatosta	Aar10505 Pamoate o	Aar26369 Somatosta	Aar27185 Somatosta	Aar27187 Somatosta	Aar27197 Somatosta	Aar23952 LH-RH, so
SUMMARIES	ID	ABP53965	AAY76794	ABP53964	ABP53418	ADJ25834	AAW27066	ABP24270	ABP15891	ABP15892	ABP24235	AAR93713	AAU83934	AAR08140	AAY76792	ABP53416	AAP61465	AAP90981	AAR14237	AAR15362	AAR10505	AAR26369	AAR27185	AAR27187	AAR27197	AAR23952
	DB	2	ო	S	ß	æ	~	4	4	4	4	N	Ŋ	~	ო	S	-	Н	~	7	~	7	~	~	7	7
	Query Match Length	8	7	7	7	7	8	80	80	80	80	9	9	7		7	ω	œ	œ	8	8	80	80	80	80	80
a	Query Match	100.0	97.4	97.4	97.4	84.6	84.6	84.6	84.6	84.6	84.6	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1
	Score	39	38	38	38	33	33	33	33	33	33	32	32	32	32	32	32	32	32	32	32			32	32	
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	Somatosta	Lanthioni	Somatosta	Human som	Somatosta	Somatosta													
Aar40822	Aar41502	Aar32766	Aar31513	Aar31511	Aar42653	Aar56781	Aar76207	Aar76205	Aar85570	Aay02418	Aaw18454	Aaw51865	Aay22044	Aay18229	Aaw45740	Aaw97185	Adh35407	Adh68008	Adk11160
AAR40822	AAR41502	4AR32766	AAR31513	4AR31511	AAR42653	AAR56781	AAR76207	AAR76205	AAR85570	4AY02418	AAW18454	AAW51865	AAY22044	4AY18229	AAW45740	AAW97185	DH35407	DH68008	ADK11160
7	7	~	7	7	7	7 7	7	7	7		7	7		•	7 2	7	~	7	7
80	œ	œ	œ	80	80	80	80	œ	80	œ	80	80	œ	80	80	8	80	80	80
82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1
32	35	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

one building unit containing a nitrogen atom of the peptide backbone

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                   have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, represents a specifically claimed VEGFR-3 binding peptide from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Somatostatin analogue; therapy; cyclic peptide; autoimmune disease; endocrine disorder; cancer; diabetic-associated complication; diagnosis; gastrointestinal disorder; inflammatory disease; panoreatitis; atherosclerosis; restenosis; post-surgical pain; VIP secretion inhibitor; hormone-secreting tumour; hormone-dependent tumour; diarrhoea; vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyclized somatostatin analogs for inhibiting growth hormone secretion from anterior pituitary and as antiproliferative agents for the treatment
inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 39; DB 5; Length 8; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gellerman G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Somatostatin analogue peptide 3181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY76794 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Trp-NH2'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-IL000329.
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98US-00203389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Afargan MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-136888/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GYWXXXWX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYWXXXWX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY76794
AAY
883666666666668888
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This sequence represents a somatostatin analogue of the invention. The invention relates to a backbone cyclised somatostatin analogue that has

Example 11; Page 61; 82pp; English.

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connected to a bridging group comprising an amide, thioether, thioester or disulphide. At least one building unit is connected via a bridging group to form a cyclic structure with a moiety selected from a second building unit, side chain of or N-terminal amino acid residue. A composition containing the analogue may be used for preventing disorders uch as cancers, autoimmune diseases, endocrine disorders, inflammatory associated complications, gastrointestinal disorders, inflammatory diseases, pancreatitis, atherosclerosis, restenosis and post-surgical associated complications, gastrointestinal disorders, inflammatory diseases, pancreatitis, atherosclerosis, restenosis and post-surgical analogues can be used for diagnosing cancer. The backbone cyclic analogue is used for imaging the existence of metatases. Somatostatin analogues can be used for the treatment patients with hormone-secreting analogues can be used for the treatment patient arity with hormone-secreting inhibition of vasoactive intestinal peptide (VIP) secretion and by direct effect on intestinal secretion. Somatostatin analogues selective to type 2 and 5 receptors may be used for treatment of non-insulin dependent diabetes mellitus. They are useful for the prevention of atherosclerosis and restenosis. The analogues are metabolically stable, selective in their in-vivo activities and safe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; anglogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 3; Length 7; Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4..6
/note= "X is any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEGFR-3 binding peptide SEQ ID NO:67.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP53964 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kubo H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JAN-2002; 2002WO-IB000099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JAN-2001; 2001US-0262476P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                97.48;
57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alitalo K, Koivunen E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LICH ) LICENTIA LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GYWXXXW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||:::|
1 GYWKVCW
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP53964;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
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ADJ25834;
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                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                 have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGRR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                   to and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endocrine disorder; inflammation; gastrointestinal disorder; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic; somatotropin release inhibiting factor; somatostatin receptor subtype; synthesis; antiatrariosclerotic; immunosuppressive; cytostatic; cancer; antidiabetic; antiinflammatory; somatostatin receptor ligand; atherosclerosis; autoimmune disease; diabetic-associated complication;
                                The present invention describes an isolated peptide (I) that binds to inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
                                                                                                                                                                                                                                              Gaps
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0
                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                       Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "N-terminally modified with Fmoc
                                                                                                                                                                                                                      97.4%; Score 38; DB 5; Le
100.0%; Pred. No. 1.7e+06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                              Backbone cyclised somatostatin analogue PTR 3181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (fluorenylmethoxycarbonyl) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "D form residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
           Claim 21; Page 81; 149pp; English.
                                                                                                                                                                                                                                                                                                                                            ABP53418 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pancreatitis; post-surgical pain.
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                                                                                                                                                                                                                                                                                                                                                                                       19-NOV-2002 (first entry)
                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hornik V, Afargan MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HORN/) HORNIK V.
(AFAR/) AFARGAN M M.
(GELL/) GELLERMAN G.
                                                                                                                                                                                                                                                                              GYWXXXW 7
                                                                                                                                                                                                                                                                  GYWXXXW 7
                                                                                                                                                                             present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2002052315-A1
                                                                                                                                                                                                 Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-DEC-1998;
15-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                  ABP53418;
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The present invention describes backbone cyclised somatostatin analogues at the timocoporates at least one building unit containing one nitrogen atom of the peptide backbone connected to a bridging group (comprising an amide, thioether, thioester or disulfide) where at least one building unit is connected via the bridging group to form a cyclic structure with a side chain of an amino acid residue of the sequence or the N-terminal amino acid residue. (1) has antiarteriosclerotic, immunosuppressive, cytostatic, antidiabetic, antianflammatory and analgesic activities, and treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   associated complications, endocrine disorders, inflammation, gastrointestinal disorders, pancreatitis, post-surgical pain, and restenosis. (1) can also be used in the diagnosis of cancer, by imaging the existence of metastases, it being labeled with a detectable probe. The present sequence represents a backbone cyclised somatostatin analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identification of ligand that can mediate biological activity of target protein, comprises screening first combinatorial library having first member ligands for binding to target protein to identify target-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
                                                                the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                         New backbone cyclized somatostatin analogs are e.g. useful in treatment of atherosclerosis, autoimmune diseases and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ligand identification; peptide library; cyrosine tRNA synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 5; Length 7;
Pred. No. 1.7e+06;
3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tyrosine tRNA synthetase binding peptide group 2 motif
                                                                                                                                                       Example 12; Page 21; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADJ25834 standard; peptide; 7 AA.
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97WO-US019638.
98US-00050359.
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57.1%;
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Best Local Similarity 57.1°
----- 4; Conservative
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WPI; 2002-681319/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-068186/07.
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GYWKVCW 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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ABP24270;
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                                                  The invention relates to a method of identifying a ligand that can mediate the biological activity of target protein via inhibition of the binding of target protein to a binding partner ligand comprising screening first combinatorial library having first member ligands for binding to target protein to identify target-binding ligands for method is useful for identifying ligands that can mediate the biological activity of target proteins via inhibition of the binding of target proteins used as reagent. The need for the natural binding partner be used as reagent. The natural binding partner sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Galactanase; fruit juice; vegetable juice; wine; pectin; depectinisation; animal feed; foodstuff.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fungal galactanase and related DNA - useful in animal feed industry and fruit juice depectinisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynascus heterothallicus; strain CBS 117.65.
Humicola insolens; strain DSM 1800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
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   Example 5; SEQ ID NO 94; 98pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.6%;
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96DK-00000235
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Best Local Similarity 42...
3, Conservative
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YWWPDWG 7
                                                                                                                                                                                                                                                                                                                                                                                                 present invention.
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AAW270666
AAW270666
AAW27066
AAW2706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABPLISO1 to ABPS5412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
MAR-2003 to correct PI field.) (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1.
                                                                                                                                                          Gaps
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                                                                                                                   Score 33; DB 2; Length
Pred. No. 1.7e+06;
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Kubo RT, Grey HM;
                                                                                                                                                            4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                   ABP24270 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV A24 motif pol peptide #78.
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                                                                                                                   84.6%;
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                                                                                                                                                            3; Conservative
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Baker DM, Celis E,
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                                                                                                                   Query Match
Best Local Similarity
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2 YWEPAWI
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                                                                          Sequence 8 AA;
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Gaps ; 0

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HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
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                            Score 33; DB 4; Lengtn e;
Pred. No. 1.7e+06;
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Kubo RT, Grey HM;
                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV A24 super motif pol peptide #71.
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                                                                                                                                                                                                                                                                                                                                                     ABP15891 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus 1.
                                                     84.6%;
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(first entry)
                                                                                                           3; Conservative
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Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIM-) EPIMMUNE INC.
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                                          Query Match
Best Local Similarity
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                                                                                                                                                                                             ||:::|:
2 YWQATWI
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Sequence 8 AA;
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15-JUL-2002
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Baker DM,
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                                                                                                        Matches
                                                                                                                                                                                                                                                                                               RESULT 8
ABP15891
ABP15891
ABP15891
ABP17
AX
ABP1 11-S
DT 11-S
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The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequences selected from 51 defined amino acid sequences (ABL2347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, and proup-based vaccine may be selected from conserved regions of viral or an group-based vaccine may be selected from conserved regions of viral or an entigens. Purhermore, immunospenseive groups for inclusion in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to composition of the groups, for Land HTL), and further, to modify the composition of the groups, the immune response can be modulated, as appropriate, for the target disease. Similar enginearing of the response is not possible with traditional approaches can be modulated, as appropriate, for the target disease. Similar enginearing of the present represent peptide sequences used in the exemplification of the present represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)

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Sequence 8 AA
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the present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequences delected from 51 defined amino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen in group-based vaccine may be selected from conserved regions of viral crumour-associated antigens, which therefore reduces the likelihood of the antigens. Purthermore, immunospenseive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP155112 represent ceptures used in the examplification of the present represent epeptide sequences used in the examplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field) ö HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte, CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide. Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1. Gaps ö Score 33; DB 4; Length 8; Pred. No. 1.7e+06; 4; Mismatches 0; Indels Livingston BD, Southwood S, Livin Kubo RT, Grey HM; HIV A24 super motif pol peptide #72. Claim 32; Page 194; 448pp; English. ABP15892 standard; peptide; 8 AA. Human immunodeficiency virus 1. 84.6%; 05-OCT-2000; 2000WO-US027766. 99US-00412863. (first entry) Best Local Similarity 42.9 Matches 3; Conservative (revised) Sidney J, Celis E, (EPIM-) EPIMMUNE INC WPI; 2001-354887/37 2 YWXXXWX ||:::|: 2 YWQATWI WO200124810-A1 Sequence 8 AA; 05-OCT-1999; 11-SEP-2003 15-JUL-2002 12-APR-2001 Sette A, Baker DM, ABP15892; Query Match ABP15892 ઠ 셤

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2 YWXXXWX 8
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2 YWQATWI
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                                                                                                                                                                                                                                                                                         Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LO-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                            WO9521187-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful e.g.
                                                                                                                                                                 10-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-AUG-1995.
                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                       AAR93713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
                                                                                 RESULT 11
                                                                                                AAR93713
                                      원
                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequences selected from 51 defined amino acid sequences (ABL23347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole articles is directed largely toward variable regions of the antigen, antigens is directed largely toward variable regions of the antigen, callowing for immune secape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or an group-based vaccine may be selected from conserved regions of viral or an entigens. Which therefore reduces the likelihood of the mountains. Burkhermore, immunesuppressive groups fart may be present or in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. Application of the present represent peptide sequences used in the examplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)
                ö
                                                                                                                                                                                                                                                           HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1.
                Gaps
                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chesnut R;
Pred. No. 1.7e+06;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Southwood S, Livingston BD, Kubo RT, Grey HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 32; Page 366; 448pp; English
                                                                                                                                       ABP24235 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus 1
                                                                                                                                                                                                                                   HIV A24 motif pol peptide #43.
                                                                                                                                                                                                                                                                                                                                                                                                 35-OCT-2000; 2000WO-US027766
                                                                                                                                                                                                                                                                                                                                                                                                                            99US-00412863
42.9%;
                                                                                                                                                                                           (revised)
(first entry)
               3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sidney J,
Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-354887/37.
                                       YWXXXWX 8
                                                        ||:::|:
YWQATWI 8
 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              WO200124810-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                              05-OCT-1999;
                                                                                                                                                                                          11-SEP-2003
15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                        12-APR-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sette A,
Baker DM,
                                                                                                                                                                 ABP24235;
               Matches
                                                                                                           RESULT 10
                                                                                                                          ABP24235
                                                                  셤
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                                                                                                                                                                                                                                                                                                                                              /note= "not an N-terminal amino acid, but condensed with Trp(6) to form a cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New cyclic peptide derivs. - are neurokinin A and tachykinin antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "not a C-terminal amino acid, but condensed with Tyr(1) to form a cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The patent describes novel cyclic hexapeptide and octapeptide compounds which are antagonists of neurokinin A and which are useful medically as analgesics and for treating respiratory diseases such as asthma. The present sequence represents a specifically preferred example of the new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                   neurokinin A antagonist; tachykinin; respiratory disease; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB 2; Length 6; Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for treating asthma or as analgesics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harbeson SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      note= "D-form residue"
                                                                                                                                                                                                                                                                                                 Location/Qualifiers
AAR93713 standard; peptide; 6 AA.
                                                                                                                                        Cyclo[-Tyr-trp-Leu-Arg-Gly-Trp-]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU83934 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buck SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Page 69; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (RICH ) MERRELL DOW PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-00191571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95WO-US000296.
                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Owen TJ, Kudlacz EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-336695/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                           analgesic; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 YWXXXW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||:::|
YWLRGW
                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU83934;
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ID AAUE
XX
AC AAUE
XX
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Gaps

; 0

Score 33; DB 4; Length 8; Pred. No. 1.7e+06; 4; Mismatches 0; Indels

Query Match
Best Local Similarity 42.9%;
Matches 3; Conservative

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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             Meli A;
                                                                                                                                                                                                                                                                                                                                                                       WPI; 1990-363658/49.
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nes 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | : : : |
2 YWVWWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 YWXXXW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   urinary bladder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7 AA;
                 Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                           Modified-site
                                                                                       Modified-site
                                                                                                                       Modified-site
                                                                                                                                                                                                                                  25-MAY-1990;
                                                                                                                                                                                                                                                               29-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9965508-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-APR-2000
                                                                                                                                                                                                     05-DEC-1990.
                                                                                                                                                                                                                                                                                                                                           Giuliani S,
                                                                                                                                                                      EP401177-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY76792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY76792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         원
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The method relates to a method of identifying a modulator of cell growth, comprising assessing and comparing the activities of site-specific DNA recombinase (I) or type I DNA topoisomerase (II) in presence and absence of a test substance. A difference in activity of (I) and (II) assessed in the presence and absence of the test substance indicates that the test substance modulates cell growth. The identified cell growth modulator, preferably an inhibitor of (I) or (II), is useful for inhibits cell growth in a subject, preferably a human. The inhibitor inhibits (I) which is preferably tyrosine recombinase or type I DNA topoisomerase in humans that proving or suspected of having tumour or cancer, where the method further involves administering an effective of antitumour or anticancer agent or treatment; or who are, or are suspected of being infected by a bacterium, in which case the inhibitor inhibits Holliday junction intermediate in which case the inhibitor inhibits Holliday junction intermediate administering an effective amount of antibiotic or antibacterium administering an effective amount of antibiotic or antibacterium treatment. AAU83898-AAU83991 represents tyrosine recombinase inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                          Tyrosine recombinase; antibacterial; cytostatic; cell growth modulator; site-specific DNA recombinase; type I DNA topoisomerase; tumour; tyrosine recombinase; cancer; Holliday junction.
                                                                                                                                                                                                                                                                                                                                                                           growth in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                        Identifying cell growth modulators for inhibiting cancer cell growth humans, involves assessing and comparing activity of site-specific recombinase or type I DNA topoisomerase in presence/absence of test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ub .,
1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.1%; Score 32; DB 5; Length 6; 50.0%; Pred. No. 1.7e+06; ive 3; Mismatches 0; Indels
                              Tyrosine recombinase inhibitory peptide #37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NK-2-receptor; bronchoconstriction; spasm.
                                                                                                                                                                                                                                                                                 (UYSA-) UNIV SAN DIEGO STATE FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 39; Page 90; 115pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR08140 standard; protein; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurokinin A peptide antagonist.
                                                                                                                                                                                                                  21-JUN-2001; 2001WO-US020046
                                                                                                                                                                                                                                                 22-JUN-2000; 2000US-00602087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-FEB-1991 (first entry)
08-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 50.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                Pinilla C;
                                                                                                                                                                                                                                                                                                                                              WPI; 2002-114591/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YWXXXW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YWCYWW
                                                                                                                                                        WO200198540-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6 AA;
                                                                                                                                                                                     27-DEC-2001.
                                                                                                                                                                                                                                                                                                                Segall A,
                                                                                                                                                                                                                                                                                                                                                                                                                          substance.
                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR08140;
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g

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Somatostatin analogue; therapy; cyclic peptide; autoimmune disease; endocrine disorder; cancer; diabetic-associated complication; diagnosis; gastrointestinal disorder; inflammatory disease; pancreatitis; atherosclerosis; restenosis; post-aurgical pain; VIP secretion inhibitor; hormone-secreting tumour; hormone-dependent tumour; diarrhoea; vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide antagonists of the NK-2-receptor of neurokinin A are useful in the treatment of Bronchoconstrictions or spasms of the intestines or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic peptide antagonists of neurokinin A - solid phase synthesis, active against bronchoconstricting or spasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pestellini V, Maggi CA, Patacchini R, Santicioli P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 2; Length 7; Pred. No. 1.7e+06; 3; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Somatostatin analogue peptide 3177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY76792 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Trp-NH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 7; 9pp; English
/label= D-Trp
                                                                                                                 label= D-Trp
                                                                                                                                                                           /label= D-Trp
                                                                                                                                                                                                                                                                                                                                                          90EP-00830234.
                                                                                                                                                                                                                                                                                                                                                                                                                  89IT-00009432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MENA ) MENARINI A IND FARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                          label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
```

/note= "D form residue"

Misc-difference 3

Modified-site

/note= "amidated"

US2002052315-A1

02-MAY-2002

13-DEC-2000; 2000US-00734583.

98US-00100360. 98US-00203389. 99WO-IL000329

19-JUN-1998; 02-DEC-1998; 15-JUN-1999;

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This sequence represents a somatostatin analogue of the invention. The invention relates to a backbone cyclised somatostatin analogue that has connected to a bridging a nitrogen atom of the peptide backbone connected to a bridging group comprising an amide, thioether, thioester or disulphide. At least one building unit is connected via a bridging group comprising an amide, thioether, thioester or disulphide. At least one building unit is connected via a bridging group to form a cyclic structure with a moiety selected from a second building unit, side chain of or Neterminal amino acid residue. A composition containing the analogue may be used for preventing disorders such as cancers, autofinmune diseases, endocrine disorders, diabeticases composition complications, gastrointestinal disorders, inflammatory diseases, pancreatitis, atherosclerosis, restenosis and post-aurgical pain. It may also be used for diagnosing cancer. The backbone cyclic analogues can be used for imaging the existence of metastases. Somatostatin analogues can be used for the treatment patients with hormone-secreting analogues can be used for the treatment patients with hormone-secreting inhibition of vasoactive intestinal peptide (VIP) secretion and by direct effect on intestinal secretion. Somatostatin analogues selective to type of an analogue selective intestinal for the prevention of atherosclerosis and restenosis. The analogues are metabolically stable, selective in their in-vivo activities and safe metabolically stable, selective in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyclized somatostatin analogs for inhibiting growth hormone secretion from anterior pituitary and as antiproliferative agents for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gellerman G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 11; Page 61; 82pp; English
                                                                                               99WO-IL000329.
                                                                                                                                                                                               98US-00100360,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Afargan MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-136888/12
                                                                                                                                                                                                                                                                                                                                       (PEPT-) PEPTOR LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7 AA;
                                                                                               15-JUN-1999;
                                                                                                                                                                                               19-JUN-1998;
                                                                                                                                                                                                                                            02-DEC-1998;
23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                  Hornik V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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New backbone cyclized somatostatin analogs are e.g. useful in the treatment of atherosclerosis, autoimmune diseases and cancers.

Example 12; Page 21; 30pp; English.

Hornik V, Afargan MM, Gellerman G;

WPI; 2002-681319/73

(HORN/) HORNIK V. (AFAR/) AFARGAN M M. (GELL/) GELLERMAN G.

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The present invention describes backbone cyclised somatostatin analogues

(1) that incorporates at least one building unit containing one nitrogen

atom of the peptide backbone connected to a bridging group (comprising an

anide, thiosether, thioseter or disulfide) where at least one building

unit is connected via the bridging group to form a cyclic structure with

c a moiety selected from the group consisting of a second building unit,

the side chain of an amino acid residue of the sequence or the N-terminal

c anino acid residue. (I) has antiarteriosolerotic, immunosuppressive,

cytostatic, antidiabetic, antiinflammatory and analgesic activities, and

cc can be used as a somatostatin receptor ligand. (I) are useful in the

c treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-

associated complications, endocrine diseases, inflammation,

construction also be used in the diagnosis of cancer, by imaging

the existence of metastases, it being labeled with a detectable probe.

The present sequence represents a backbone cyclised somatostatin analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.1%; Score 32; DB 5; Length 7; 50.0%; Pred. No. 1.7e+06; ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.00,
Best Local Similarity 50.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.1%; Score 32; DB 3; Length 7; 50.0%; Pred. No. 1.7e+06; ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP53416 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 YWXXXW 7
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2 YWKVCW 7
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Gaps

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Search completed: January 3, 2005, 17:32:20

Job time : 156 secs

Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic; somatotropin release inhibiting factor; somatostatin receptor subtype; synthesis; antiarteriosclerotic; immunosuppressive; cytostatic; cancer; antidiabetic; antilnilammatory; somatostatin receptor ligand; atherosclerosis; autoimmune disease; diabetic-associated complication; endocrine disorder; inflammation; gastrointestinal disorder; restenosis;

Location/Qualifiers

pancreatitis; post-surgical pain

Synthetic

Key

Backbone cyclised somatostatin analogue PTR 3177.

(first entry)

19-NOV-2002

ABP53416;

RESULT 15 ABP53416

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Matches

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US-09-069-827A-94
Sequence 5, Appli
Sequence 6, Appli
Sequence 12, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 30, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 6, Appli
                                                                                                       (without alignments)
14.339 Million cell updates/sec
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                                                                                         ; Search time 37 Seconds
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-100-804-5

US-09-100-804-5

US-09-091-45-5

US-08-951-260A-2

US-08-81-260A-1

US-08-884-569A-11

US-08-884-569A-11

US-09-36-626A-2

US-09-743-492A-4

US-09-743-492A-4

US-09-743-235A-30

US-08-652-971-5

US-08-991-558A-5

US-08-991-558A-5

US-08-991-558A-5

US-08-991-53A-5

US-08-991-953A-5

US-08-991-953A-5

US-08-991-953A-5

US-08-467-472C-6
                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-384-061-5
US-09-384-061-6
US-09-384-061-7
US-09-384-061-8
                                                                                                                                                                                                                                       478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
                                                                                       January 3, 2005, 17:27:19
                                                                                                                                                                                                BLOSUM62DX Gapext 0.5
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                                                                                                                                           US-10-046-922-68
39
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Match Length
                                                                                                                                                                      1 GYWXXXWX 8
                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                       Run on:
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Appli
                                 Sequence 5, A
Sequence 7, A
Sequence 1, A
Sequence 1, A
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Sequence
Sequence
Sequence
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Sequence
Sequence
 Sequence
                 Sequence
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FOURTES, Dana M

KAY, Brian K

FRELINGER, Jeffrey A

HYDE-DERUYSCHER, Robin P

TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING

COMPLEMENTARY COMBINATORIAL LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDLUM TYPE Floppy disk

COMPUTER: Propagatible

COMPUTER: ISP Compatible

COMPUTER: ISP Compatible

COMPUTER: ISP Compatible

COMPUTER: ISP Compatible

COMPUTER: ISP COMPATIBLE SACTORIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/069,827A

FILING DATE: 30-Apr-1998

APPLICATION NUMBER: US 09/050,359

FILING DATE: 31-AAR-1998

APPLICATION NUMBER: PCT/US97/19638

FILING DATE: 31-CT-1997

ATTORNAY AGENT INFORMATION:

AND ATTORNAY AGENT INFORMATION:

AND ATTORNAY AGENT INFORMATION:

AND ATTORNAY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street N.W., Suite 300
CITY: Weakington
STATE: D.C.
           US-09-194-832-1
US-09-852-870A-5
US-09-852-870A-7
US-09-652-868-1
US-09-552-868-1
US-09-552-868-1
US-08-488-659A-67
US-09-553-22C-53
US-09-563-22C-53
US-08-956-670A-17
US-09-780-070-5
US-08-958-670A-17
US-09-10-552-42
US-08-353-400-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: FOWLKES=4C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 94, Application US/09069827A Patent No. 6617114 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN TITLE OF INVENTION: TYROSINE PHOSPHATASES CORRESPONDENCES: 34
CORRESPONDENCE ADDRESS: ADDRESSER: MOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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; Sequence 5, Application US/09081345
; Patent No. 6226641
; GENERAL INFORMATION:
    APPLICANT: Babija Jallal
; APPLICANT: Gregory D. Plowman
TITLE OF INVENTION: PTP04 RELATED DISORDERS;
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 Weer Fifth Street
; STREET: Suite 4700
                                                                                                                                                                                                                                                                                      ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IOCATION: 5
OTHER INFORMATION: /note= "Xaa = I or V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/596,291
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
FILING APPLICATION NUMBER: PCT/US94/09943
FILING ATTORNATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: LO461/7003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 611-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                         STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide HYPOTHETICAL: NO
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1 FWRMXWE 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-100-804-5
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                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-08-443-640-16
US-08-443-640-16
Sequence 16, Application US/08443640
Sequence 16, Application US/08443640
Sequence 16, Application US/08443640
SEQUENCE 10 SEQUENCE
                                                                                                                                       Gaps
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0
                                                                     84.6%; Score 33; DB 4; Length 7; 42.9%; Pred. No. 3.8e+05; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 7;
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Sequence 5, Application US/09100804

Sequence 5, Application US/09100804

Patent No. 606647-6

APPLICANT: GONEZ, LEONEL JORGE

APPLICANT: SARAS, JAN

APPLICANT: CLASSSON-WELSH, LENA

APPLICANT: HELDIN, CARL-HENRIK

TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATORNING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,640
FILLING DATE: 18-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 29; DB 1; Pred. No. 3.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-102
TELEPHONE: (508) 927-5054
TELEPHONE: (508) 927-5054
TELEPHONE: (508) 927-105
INPORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 42.9%;
Matches 3; Conservative
                                    Query Match
Best Local Similarity 42.9%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                      2 YWXXXWX 8
                                                                                                                                                                                                                                       | | ::: | :
YWWPDWG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | |:::|
1 GEWRFAW 7
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         US-09-069-827A-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-443-640-16
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APPLICATION NUMBER: US/09/095,443 FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COTHER INFORMATION:
COTHER INFORMATION:
COTHER INFORMATION:
COTHER INFORMATION:
US-09-043-6
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 YWXXXWX 8 : | | : | | |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: "Xaa" in positions 4 and 6 stand OTHER INFORMATION: for an unspecified amino acid. OTHER INFORMATION: "Xaa" in position 8 stands for OTHER INFORMATION: either Glu or Asp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-01-05-443-6

Sequence 6, Application US/09095443

Sequence 6, Application US/09095443

Patent No. 6342593

GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
APPLICANT: Peles, Eior
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: OF ALP RELATED DISORDERS
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
ADDRESSE:
STREET: 633 Weet Fitch Street
STREET: 631 Weet Fitch Street
                              COUNTRY: U.S.A.

ZIP: 90071-2066
COUNTRY EXADABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 6.00 SOFTWARE: 1.84 COMPUTER READABLE FORM:
COMPUTER PREADABLE FORM:
MEDIUM TYPE: 6.00 SOFTWARE: 18M COMPATALIBLE OPERATING SYSTEM: 1BM P.C. DOS 5.0 SOFTWARE: FASTENG FOR WINDOW 2.0 CURRENT APPLICATION NUMBER: US/09/081,345 FILING DATE: Herewith CLASSIPTCATION NUMBER: 60/047,222 FILING DATE: MAY 20, 1997
ATTORNEY AGENT INPORMATION:
NAWE: WALDER REPREMENTS RECISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
RELECHONE: (213) 955-0440
TELECHONE: (213) 955-0440
TELECHO FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
Los Angeles
California
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2 FWXMXWX B
                         STATE: CA
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Gaps
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74.4%; Score 29; DB 3; Length 8;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Xaa" in positions 4 and 6 stand
for an unspecified amino acid.
"Xaa" in position 8 stands for
either Glu or Asp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12. Application US/08446345; Patent No. 5831009; GENERAL INFORMATION:
APPLICANT: Ullrich, Axel APPLICANT: Ullrich, Axel APPLICANT: Moller, Karin B. TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE TITLE OF INVENTION: PHOSPHATASES PTP-D1 NUMBERS OF SEQUENCES: 41
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: Pennie & Edmonds STRET: 1155 Avenue of the Americas CITY: New York STATE: N.Y.
COUNTRY: U.S.A.
ZITY: 10036-2711
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,345
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION THE STATE OF THE STATE 
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REGISTRATION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 7683-054
TELECOMMUNICATION INFORMATION:
FILING DATE: Herewith CLASSIFICATION PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: PILING DATE: June 12, 1997, ATONNEY/AGENT INFORMATION: NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327, REPRENGE/DOCKET NUMBER: 235/055 TELECOMMUNICATION INFORMATION: TELEPAX: (213) 955-0440

TELEPAX: (213) 955-0440
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| Sequence 11, Application US/08884569A |
| Sequence 11, Application US/08884569A |
| Patent No. 6399326 |
| GENERAL INFORMATION: |
| APPLICANT: CHIANG, MING-KO |
| APPLICANT: FLANAGAN, JOHN G. |
| TITLE OF INVENTION: RECEPTOR TYROSINE PHOSPHATASE, AND USES RELATED THERETO |
| TITLE OF INVENTION: RECEPTOR TYROSINE PHOSPHATASE, AND USES RELATED THERETO |
| CURRENT APPLICATION NUMBER: US/08/84,569A |
| CURRENT FILING DATE: 1997-06-27 |
| PRIOR PRIOR FILING DATE: 1996-07-02 |
| NUMBER OF SEQ ID NOS: 15 |
| SEQ ID NO 11 |
| LENGTH: 6 |
| LENGTH: 
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Sequence 14, Application US/08884569A

Patent No. 6399326

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: CHIANG, MING-KO

APPLICANT: CHIANG, MING-KO

APPLICANT: FLANAGAN, JOHN G.

TITLE OF INVENTION: RECRETYOR TYROSINE PHOSPHATASE, AND USES RELATED THERETO

TITLE OF INVENTION NUMBER: US/08/884,569A

CURRENT FILING DATE: 1997-06-27

PRIOR APPLICATION NUMBER: 60/021,040

PRIOR PAPLICATION NUMBER: 60/021,040

PRIOR PRIOR PAPLICATION NUMBER: 2.1

SOFTWARE: PARCHIN Ver. 2.1

SEQ ID NO: 14

LENGTH: 6
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NAME/KEY: MOD_RES
LOCATION: (3)
OTHER INFORMATION: Arg or Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
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Score 28; DB 3; Length 6; Pred. No. 3.8e+05; 2; Mismatches 0; Indels
        71.8%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: MOD_RES
LOCATION: (5)
CTHER INDERMATION: 11e or Val
US-08-884-569A-11
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ORGANISM: Artificial Sequence
FEATURE:
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OTHER INFORMATION: Ile or Val
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    Query Match 71.8
Best Local Similarity 66.7
Matches 4; Conservative
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                                                                                                                                                                                                          :||:||
1 FWXMXW 6
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1 FWRMXW 6
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Patent No. 6004791
GENERAL INFORMATION:
APPLICANT: Aoki, Naohito
APPLICANT: Avei
TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
TITLE OF INVENTION: AND RELATED PRODUCTS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: "Xaa" in positions 3 and 5 stand; OTHER INFORMATION: for an unspecified amino acid. US-08-951-260A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Sulte 4.vu
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: BASESQ for Windows 2.0
SOFTWARE: ESECRED for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,260A
FILING DATE: October 16, 1997
CLASSIFICATION NUMBER: 60/030,860
FILING DATE: No. 6004791ember 13, 1996
APPLICATION NUMBER: PCT/1897/00946
FILING DATE: June 17, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
RELERENCE/DOCKET NUMBER: 32,327
REGISTRATION NUMBER: 32,3327
REG
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STREET: 633 West Fifth Street
STREET: Suite 4700
                                             TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
                (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown MOLECULE TYPE: peptide
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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1 FWXMXW 6
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US-08-951-260A-2
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                TELEFAX:
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OTHER INFORMATION: Description of Artific OTHER INFORMATION: Sequence NAME/KEY: MOD_RES LOCATION: (3)—OTHER INFORMATION: Variable amino acid NAME/KEY: MOD_RES LOCATION: (5)—OTHER INFORMATION: Variable amino acid OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/09743492A Patent No. 6709843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial sequence
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Matches 4; Conservative
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1 FWXMXW 6
  FWXMXW 6
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US-09-743-492A-5
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                                                                                  Gaps
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                                                                                                                                                                                                                                                         Sequence 2, Application US/09430626A
Sequence 2. Application US/09430626A
Batent No. 6482605
GENERAL INFORMATION:
APPLICANT: AOKi, Nachito
TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
AND RELATED PRODUCTS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 71.8%; Score 28; DB 4; Length 6; Best Local Similarity 66.7%; Pred. No. 3.8e+05; Matches 4; Conservative 2; Mismatches 0; Indels
                                        Length 6;
                                      71.8%; Score 28; DB 3; I
66.7%; Pred. No. 3.8e+05;
tive 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P. C. DOS 5.0
SOFTWARE: FASTENG for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,626A
FILING DATE: 29-OCC-1999
CLASSIFICATION: «UKANOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/951,260
FILING DATE: October 16, 1997
APPLICATION NUMBER: 60/030,860
FILING DATE: No. 6482605ember 13, 15
APPLICATION NUMBER: PCT/1897/00946
FILING DATE: June 17, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warburg, Richard J.
REGISTRATION VUMBER: 32,327
REFERENCE/DOCKET NUMBER: 227/004
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acide
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
                     Query Match
Best Local Similarity 66.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                         :||:||
1 FWXMXW 6
                                                                                                                      2 YWXXXW 7
US-08-884-569A-14
                                                                                                                                                                                                                         RESULT 10
US-09-430-626A-2
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Gaps

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GENERAL INFORMATION:

APPLICANT: YAMAMOTO, Hiroshi

APPLICANT: YAMAMOTO, Wikko

APPLICANT: TSUJIKAWA, Kazutake

APPLICANT: UCHINO, YUKIKO

TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR INTRACELLULAR DOMAIN OF PROTEIN

TITLE OF INVENTION: TYROSINE PHOSPHATASE

TITLE OF INVENTION: TYROSINE PHOSPHATASE

TITLE OF INVENTION: TYROSINE PHOSPHATASE

CURRENT PILING DATE: 2001-04-30

PRIOR PAPLICATION NUMBER: PCT/JP98/03120

PRIOR PLING DATE: 1998-07-10

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PALENTING DATE: 2.0

SEQ ID NO 5

LENGTH 6

LENGTH 6
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Sequence 46, Application US/09361096A

Sequence 46, Application US/09361096A

Patent No. 6492495

GENERAL INFORMATION:

APPLICANT: MOLLER, NIELS P.H.

APPLICANT: MOLLER, AXEL

TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE

FILE REPERENCE: 038602/0686

CURRENT FILING DATE: 1999-07-26

CURRENT FILING DATE: 1999-07-26

PRIOR PAPLICATION NUMBER: 08/036,210

PRIOR APPLICATION NUMBER: 08/036,210

PRIOR APPLICATION NUMBER: 08/036,210

PRIOR APPLICATION NUMBER: 08/036,210

SPROR FILING DATE: 1995-03-23

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PROFILING OF SEQ ID NOS: 53

SEQ ID NO 46
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OTHER INFORMATION: Description of Unknown Organism: Consensus Amino
OTHER INFORMATION: Acid Sequence in Cytoplasmic Domain of Known PTPs.
Patent No. 6709843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description of Artificial Sequence: Consensus sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.8%; Score 28; DB 4; Length 6; 66.7%; Pred. No. 3.8e+05; ive 2; Mismatches 0; Indels
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Sequence 5, Application US/08652971
Patent No. 5814507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.8%;
              Query Match
Best Local Similarity 66.7*
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 71.8
Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GYWXXXW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGWSKSW 7
                                                                                                         :||:||
1 FWXMXW 6
                                                                                       2 YWXXXW 7
                                                                                                                                                                                                                                Patent No. 5491130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-973-235A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-652-971-5
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                                                                                                                                                               Gaps
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                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                JULEARY DEFORMED TO SEQUENCE 2, Application US/10243687

Patent No. 6797501

GENERAL INFORMATION:

APPLICANT AND MACI

TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSE: Lyon & Lyon

STREET: 633 Weet Fitch Street

Solice 4700
                                                                                                                        Score 28; DB 4; Length 6;
Pred. No. 3.8e+05;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 16-Sep-2002
CLASSIFICATION AURNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 29-Oct-1999
APPLICATION NUMBER: 08/951,260
FILING DATE: COCCODE: 16, 1997
APPLICATION NUMBER: 60/030,860
FILING DATE: NOWBER: 6797501ember 13, 1996
APPLICATION NUMBER: POTY1897/00946
FILING DATE: Unne 17, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastESQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/243,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 227/004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for an unspecified amino acid. SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                 NAME/KEY: SITE

LOCATION: (5)

COTHER INFORMATION: Xaa= Val, Ile or Cys
US-09-743-492A-5
OTHER INFORMATION: Xaa= Arg, Glu or Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       storage
                                                                                                                          71.8%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 90071-2066
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                         2 YWXXXW 7
                                                                                                                                                                                                                 : | | : | |
1 FWXMXW 6
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TOPOLOGY: linear
MOLECULE TYPE: protein
PEATURE:
NAME/KEY: Active-site
LOCATION: 1..2
O'THER INFORMATION: /note= "Let 'X' located at position
OTHER INFORMATION: 1 represent either Histidine or Aspartic Acid"
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site
| LOCATION: 6.7 | LOCATION: 7.7 | COTHER INFORMATION: 6 represent either Isoleucine or Valine."
| US-08-652-971-5 
STATE: California

COUNTRY: United States

ZIP: 94080
COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,971
FILING DATE:
CLASSIFICATION TOWNER: PIO33
TELESSIFICATION NUMBER: PIO33
TELEFRANIC/DOCKET NU
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ö Query Match 71.8%; Score 28; DB 2; Length 7; Best Local Similarity 50.0%; Pred. No. 3.8e+05; Matches 3; Conservative 3; Mismatches 0; Indels

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Gaps

2 YWXXXW 7 g ઠે

:|::|| 2 FWRMXW 7

Search completed: January 3, 2005, 17:36:59 Job time : 38 secs

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Sequence 5, Appli Sequence 7, Appli Sequence 1, Appli Sequence 1, Appli Sequence 143, App Sequence 143, App Sequence 143, App

3, Appli 1, Appli 3, Appli 1, Appli 1, Appli

Sequence 3 Sequence 3 Sequence 3 Sequence Seguence Sequence

Sequence 1, Ap Sequence 143,

Sequence 153, App Sequence 1, Appli Sequence 2, Appli Sequence 46, Appl Sequence 65, Appl Sequence 76, Appli Sequence 76, Appli

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Sequence 68, Application US/10046922;
Publication No. US20020164667A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
TITLE OF INVENT NO. Hajime
TITLE OF INVENTION: VEGER-3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 28967/37084A
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 68
100.0%; Score 39; DB 13;
100.0%; Pred. No. 1.5e+06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: peptide
FEATURE:
NAME/KEY: SITE
LOCATION: (4)...(6)
COTHER INFORMATION: X is any amino acid
LOCATION: (8)...(8)
COTHER INFORMATION: X is any amino acid
US-10-046-922-68
      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GYWXXXWX 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 8; Conserv
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    LENGTH:
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Sequence 48, Appl
Sequence 243, App
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Sequence 12, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                        (without alignments)
20.556 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCCMB pep:*

1: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

1: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

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1: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

1: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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1: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

1: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

1: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

1: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

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1: /cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*

1: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

1: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

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1: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

1: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

1: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
                                                                             January 3, 2005, 17:35:40 ; Search time 140 Seconds
             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-046-922-68
US-10-046-922-67
US-10-19-943-48
US-10-190-082-586
US-10-367-590-243
US-10-367-593-243
US-10-367-654-243
US-10-367-654-243
US-10-367-654-243
US-10-367-658-243
US-10-367-658-243
US-10-367-674-243
US-10-367-674-243
US-10-367-674-243
                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-095-478-12
                                                                                                                                                                                                   1599051 segs, 359727711 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                          Published Applications AA:*
                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         OM protein - protein search, using sw model
                                                                                                                                                                   BLOSUM62DX 3 Gapext 0.5
                                                                                                                         US-10-046-922-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
Match Length
                                                                                                                                             1 GYWXXXWX 8
                                                                                                                                                                                                                                               Minimum DB seq length: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                          Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
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Gaps

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Length 8; Indels

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Sequence 243, Application US/10367580

Sequence 243, Application US/10367580

Publication No. US20040071720A1

Sequence 243, Application US/10367580

Sequence 243, Application No. US20040071720A1

APPLICANT: Nothman, James E.

APPLICANT: Hartl, F. Ulxich

APPLICANT: How mee H. Alan

APPLICANT: Mark

TILE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies

FILE REFERENCE: 11746/461061

CURRENT PELLON INVENTION NUMBER: US 09/794,832

PRIOR PELLING DATE: 2001-02-27

PRIOR PELLING DATE: 1996-02-13

PRIOR PELLING DATE: 1996-02-13

PRIOR PELLING DATE: 1996-08-16

PRIOR PELLING DATE: 1996-08-16

PRIOR APPLICATION NUMBER: US 60/002,490

PRIOR APPLICATION NUMBER: US 60/002,490

PRIOR PELLING DATE: 1995-08-18

NUMBER OF SEQ ID NOS: 349

SOFTWARE: WordPerfect 8.0 for Windows

SEQ ID NO 243

TENGTH: HOW DATE: HOW DATE: HOW DEED 
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      FILE REFERENCE: P1905R1
CURRENT APPLICATION NUMBER: US/10/190,082
CURRENT FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US 60/303,634
PRIOR FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 683
SEQ ID NO 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: synthetic peptide US-10-367-580-243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-10-367-593-243
; Sequence 243, Application US/10367593
; Publication No. US20040071721A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Synthetic US-10-190-082-586
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 3; Conserv
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GLWWFPW &
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                                                                                                                                                                                                                                   LENGTH: 8
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RESULT 2
US-10-046-922-67

Sequence 67, Application US/10046922

Sequence 67, Application US/10046922

Sequence 67, Application Wo. US20020164667A1

GENERAL INFORMATION:

APPLICANT: Altalo, Kari

APPLICANT: Kubo, Hajime

7, TILLO P. INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS

FILE REFERENCE: 28967/37084A

CURRENT APPLICATION NUMBER: US/10/046,922

CURRENT FILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin version 3.0

SEQ ID NO 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 48, Application US/10418943

Publication No. US20040002441A1

GENERAL INFORMATION

APPLICANT: Segal1, Anca

TITLE OF INVENTION: PECOMBINATION MODULATORS AND METHODS

TITLE OF INVENTION: FOR PRODUCING AND USING THE SAME

FILE REFRENCE: 011443 008-999

CURRENT APPLICATION UNMBER: US/10/418,943

CURRENT FILING DATE: 2003-04-17

PRIOR APPLICATION NUMBER: 09/602,087

PRIOR APPLICATION NUMBER: 09/602,087

NUMBER OF SEQ ID NOS: 71

NUMBER OF SEQ ID NOS: 71

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.1%; Score 32; DB 15; Length 6; 50.0%; Pred. No. 1.5e+06; ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.4%; Score 38; DB 13; Length 7; 100.0%; Pred. No. 1.5e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (4)..(6) OTHER INFORMATION: X at position 4-6 is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-10-190-082-586
US-10-190-082-586
Sequence 586, Application US/10190082
Publication No. US20030148264A1
GENERAL INFORMATION:
APPLICANT: Lasky, Lawrence A.
APPLICANT: Sidhu, Sachdev S.
APPLICANT: Held, Heike A.
TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 50.0
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GYWXXXW 7
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1 YWCYWW 6
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US-10-418-943-48
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LENGTH: 6
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Gaps

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Indels

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3; Mismatches

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3; Conservative
                                                                                                       1 GYWXXXW 7
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2 GLWWFPW
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GENERAL INFORMATION
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US-10-367-658-243
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              Matches
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                                                                                                                                                                             APPLICANT: Mayhew, Mark
ITILE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
FILE REPERENCE: 11746/61012
CURRENT APPLICATION NUMBER: US/10/367,593
CURRENT FILING DATE: 2003-02-14
FRICH FILING DATE: 1998-02-13
FRICH FILING DATE: 1998-02-13
FRICH RILING DATE: 1996-08-16
FRICH APPLICATION NUMBER: PCT/US96/13363
FRICH APPLICATION NUMBER: US 60/002,490
FRICH APPLICATION NUMBER: US 60/002,479
FRICH APPLICATION NUMBER: US 60/002,479
FRICH RILING DATE: 1995-08-18
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APPLICANT: Houghton, Alan
APPLICANT: Houghton, Alan
APPLICANT: Houghton, Alan
APPLICANT: Takechi, Yoshizumi
APPLICANT: Mayhew, Mark
TITLE OP INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
FILE REFERENCE: 1746/461041
CURRENT APPLICATION NUMBER: US/10/367,594
CURRENT PILING DATE: 2003-02-14
FRIOR FILING DATE: 2000-10-05
FRIOR PPLICATION NUMBER: DCT/US96/13363
FRIOR PILING DATE: 1998-02-13
FRIOR PILING DATE: 1995-08-18
FRIOR PILING DATE: 1995-08-18
FRIOR PILING DATE: 1995-08-18
FRIOR PILING DATE: 1995-08-18
FRIOR FILING DATE: 1995-
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Pred. No. 1.5e+06;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-593-243
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Publication No. US20040071722A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 42.9%;
Matches 3; Conservative
                                                                                        Houghton, Alan
Takechi, Yoshizumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
Hartl, F. Ulrich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GYWXXXW 7
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2 GLWWFPW 8
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LENGTH: 8
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76.9%; Score 30; DB 15; Length 8; 42.9%; Pred. No. 1.5e+06;

Query Match Best Local Similarity

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APPLICANT: Hactl, r. Ullicin.
APPLICANT: Hoe, Mee H.
APPLICANT: Hoophton, Alan
APPLICANT: Houghton, Alan
APPLICANT: Houghton, Alan
APPLICANT: Takechi, Yoshizumi
APPLICANT: Takechi, Yoshizumi
APPLICANT: Maybew, Mark
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
FILE REFERENCE: 11746/461032
CURRENT APPLICATION NUMBER: US/10/367,654
CURRENT APPLICATION NUMBER: US/10/367,654
CURRENT FILING DATE: 2000-06-10
PRIOR PILING DATE: 2000-06-10
PRIOR PILING DATE: 2000-08-10
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1996-08-16
PRIOR PILING DATE: 1995-08-18
PRIOR PILING DATE: 1995-08-18
PRIOR PILING DATE: 1995-08-18
PRIOR FILING DATE: 1995-08-18
NUMBER OF SEQ 1D NOS: 349
PRIOR FILING DATE: 1995-08-18
NUMBER OF SEQ 1D NOS: 349
SEQ 1D NO 243
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Gaps
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Publication No. US20040071723A1
GENERAL INFORMATION:
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Publication No. US20040071724A1
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rothman, James B. APPLICANT: Hartl, F. Ulrich
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Matches 3; Conservative
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CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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2 GLWWFPW 8
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APPLICANT: Rothman, James E.
APPLICANT: Hartl, F. Ulrich
APPLICANT: Houghton, Alan
APPLICANT: Houghton, Alan
APPLICANT: Houghton, Alan
APPLICANT: Houghton, Alan
APPLICANT: Takechi, Yoshizumi
APPLICANT: Mayhew, Mark
FILE REFERENCE: 11146/461072
CURRENT APPLICATION NUMBER: US/10/367,668
CURRENT APPLICATION NUMBER: US 09/794,517
PRIOR APPLICATION NUMBER: US 09/794,517
PRIOR APPLICATION NUMBER: US 09/01,645
PRIOR FILING DATE: 1996-02-13
PRIOR FILING DATE: 1996-02-13
PRIOR FILING DATE: 1995-08-16
PRIOR FILING DATE: 1995-08-16
PRIOR FILING DATE: 1995-08-16
PRIOR FILING DATE: 1995-08-16
PRIOR APPLICATION NUMBER: US 60/002,490
PRIOR FILING DATE: 1995-08-18
PRIOR APPLICATION NUMBER: US 60/002,490
PRIOR APPLICATION NUMBER: US 60/002,479
PRIOR APPLICATION NUMBER: US 60/002,479
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Pred, No. 1.5e+06;
3; Mismatches 1; Indels
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PRIOR FILING DATE: 1996-08-16
PRIOR APPLICATION NUMBER: US 60/002,490
PRIOR FILING DATE: 1995-08-18
PRIOR APPLICATION NUMBER: US 60/002,479
PRIOR FILING DATE: 1995-08-18
NUMBER OF SEQ ID NOS: 349
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 349
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 243
LENCTH: 8
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; OTHER INFORMATION: synthetic peptide
US-10-367-658-243
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US-10-367-674-243
Sequence 243, Application US/10367674
Publication No. US20040127684A1
GENERAL INFORMATION:
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Publication No. US20040071725A1
GENERAL INFORMATION:
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Best Local Similarity 42.9%;
Matches 3; Conservative
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2 GLWWFPW 8
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GLWWFPW 8
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                                                                                                                                                                                             LENGTH: 8
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APPLICANT: Rothman, James E.
APPLICANT: Harti, F. Ulxich
APPLICANT: Hoe, Mee H.
APPLICANT: Houghton, Alan
APPLICANT: Takechi, Yoshizumi
APPLICANT: Maybew, Mark
APPLICANT: Maybew, Mark
IIILE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
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Gregory D. Plowman
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
PTP04 RELATED DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
76.9%; Score 30; DB 16;
Best Local Similarity 42.9%; Pred. No. 1.5e+06;
Matches 3; Conservative 3; Mismatches 1
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storage
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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/822,295
FILING DATE: 02-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                  THILE REFERENCE: 11746/4610211
CURRENT APPLICATION NUMBER: US/10/367,674
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: US 10/170,738
PRIOR FILING DATE: 2002-06-13
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1996-08-16
PRIOR PILING DATE: 1996-08-16
PRIOR PILING DATE: 1996-08-16
PRIOR PILING DATE: 1995-08-18
PRIOR PILING DATE: 1995-08-18
PRIOR PILING DATE: 1995-08-18
PRIOR PILING DATE: 1995-08-18
NUMBER OF SEQ ID NOS: 349
SEQ ID NOS: 349
SEQ ID NOS: 349
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APPLICATION NUMBER: 09/081,345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: synthetic peptide US-10-367-674-243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-822-295-5; Sequence 5, Application US/09822295; Patent No. US20020119501A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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FEATURE:
NAME/KEY: MOD_RES
LOCATION: (6)
OTHER INFORMATION: Unspecified amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (4) OTHER INFORMATION: Unspecified amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/10328953; Publication No. US20040071656A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (8) ; OTHER INFORMATION: Glu or Asp
US-10-020-215-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
FEATURE:
                                                                                                                                                                                                                                    Query Match 74.4
Best Local Similarity 71.4
Matches 5; Conservative
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                                                                                                                  OTHER INFORMATION:
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OTHER INFORMATION:
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Matches 5; Conserv
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NAME/KEY: MOD_RES
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NAME/KEY: MOD_RES
                                                                                                                                                                                                US-09-095-478-12
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US-10-328-953-9
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US-10-020-215-6
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 74.4%; Score 29; DB 9; Length 8; Best Local Similarity 71.4%; Pred. No. 1.5e+06; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPPOG AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
NAWE: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 234/253
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELERX: 67-3510
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastERQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
                                                                                                                                                                                                                                                                                                              for an unspecified amino acid. "Xaa" in position 8 stands for either Glu or Asp. SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEX: (213) 955-0440
TELEX: (7-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
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2 FWXMXWX 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-09-095-478-12
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| Sequence 6, Application US/10020215
| Publication No. US20030008347A1
| GENERAL INFORMATION:
| APPLICANT: PLOWAMA, GREGORY |
| APPLICANT: PLOWAN GREGORY |
| APPLICANT: PLOWEN OF ALP RELATED DISORDERS |
| TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF ALP RELATED DISORDERS |
| TITLE OF INVENTION: UNMBER: US/10/020,215 |
| CURRENT APPLICATION NUMBER: 09/095,443 |
| PRIOR APPLICATION NUMBER: 09/095,443 |
| PRIOR PLILING DATE: 1998-06-10 |
| PRIOR PLILING DATE: 1998-06-10 |
| PRIOR PLILING DATE: 1997-06-11 |
| NUMBER OF SEQ ID NOS: 10 |
| SOFTWARE: PATENTIN Ver. 2.1 |
| SEQ ID NO 6 |
| CONTINUED OF TAXED OF TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 8;
                                                                                                                                                                                                                                                                                                                                                                                         74.4%; Score 29; DB 10; Length 8; 71.4%; Pred. No. 1.5e+06; ive 2; Mismatches 0; Indels.
"Xaa" in positions 4 and 6 stand
for an unspecified amino acid.
"Xaa" in position 8 stands for
either Glu or Asp.
```

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APPLICANT: Wieland, Felix
APPLICANT: Wieland, Felix
APPLICANT: Wieland, Fraze-Ulrich
ITILE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
FILE REPERRENCE: 1130/46101
CURRENT APPLICATION NUMBER: US/10/328,953
FRIOR APPLICATION NUMBER: US 60/342,570
FRIOR PILING DATE: 2001-12-28
FRIOR PELING DATE: 2001-12-28
FRIOR APPLICATION NUMBER: US 60/343,884
FRIOR APPLICATION NUMBER: US 60/372,620
FRIOR APPLICATION NUMBER: US 60/372,620
FRIOR PILING DATE: 2002-04-12
FRIOR APPLICATION NUMBER: US 60/399,342
FRIOR APPLICATION NUMBER: US 60/399,342
FRIOR PILING DATE: 2002-09-28
NUMBER OF SEQ ID NOS: 331
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 9
LENGTH: 8
LENGTH: 8
TYPE: RT
ORGANISM: Artificial Sequence
FRATURE:
ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: peptide in M13 coliphage
US-10-328-953-9
OHERY MATCH
SEC LOCAL SIMIlarity 28.6%; Pred: No. 1.5e+06;
MATCHES 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
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Search completed: January 3, 2005, 17:47:30 Job time: 141 secs

2 YWXXXWX 8 : |:::|: 2 FWPFEWI 8

q

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                    Copyright
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OM protein - protein search, using sw model

January 3, 2005, 17:26:39 ; Search time 37 Seconds (without alignments) 20.804 Million cell updates/sec Run on:

US-10-046-922-68 Title: Perfect score:

1 GYWXXXWX 8 Sequence:

BLOSUM62DX 3 Gapop 10.0 , Gapext 0.5 Scoring table:

909 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:* Database :

pirl: * pir2: * pir3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	
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	Description	gut pentapeptide -		'n	(Trp	leucokinin V - Mad	cytochrome oxidase	Ω	pullulanase (EC 3.	adipokinetic hormo	adipokinetic hormo	neuropeptide - flo	Ig heavy chain CRD		alcohol dehydrogen		T-cell receptor be			T-cell receptor be	pev-kinin 2 - pena	•	hypothetical prote	H chain V-	T-cell receptor be	:e11	_	ell	T-cell receptor be	glucuronosyltransf
SUMMARIES	ID	JH0253	B35640	F41946	S21230	JS0315	T13818	PT0728	PN0649	S15422	A58641	S21663	PT0281	PT0580	866195	PT0629	PT0532	PT0519	PT0637	PT0641	PD0028	A61068	S09652	PH1602	PT0526	PT0628	PT0642	PT0722	PT0586	PX0008
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	Score	22	17	17	17	17	17	16	16	16	16	16	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15
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pev-kinin 1 - pena venom heptapeptide tryptophyllin, bas	virotoxin - destro adipokinetic hormo neuropeptide Led-C	neuropeptide Led-C adipokinetic hormo adipokinetic hormo	adipokinetic hormo red pigment-concen adipokinetic hormo	hypertrehalosemic hypertrehalosemic adipokinetic hormo	adipokinetic hormo
PD0029 A58512 A61081	AS8725 A33995 A44960	B44960 A58620 S11545	S55310 A61348 S10596	S08995 S08996 A49823	B49823
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32	3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	36 37 38	39 40 41	4 4 4 0 6 4	45

ALIGNMENTS

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Gispecides: Anguilla japonica (Japanese eel)
Cispecides: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
Ciscession: Japonica Commun. 180; 828-832, 1991
Biochem. Biophys. Res. Commun. 180; 828-832, 1991
Biochem. Biophys. Res. Commun. 180; 828-832, 1991
Biochem. Biophys. Res. Commun. 180253; MUD:92062113; PMID:1953755
A; Reference number: JH0253; MUD:92062113; PMID:1953755
A; Residues: 15 < CUES>
A; Residues: 15 < CUES>
A; Residues: 15 < CUES>
A; Residues: 16 < CUES>
A; Residues: 175 < CUES>

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Best Local Similarity 40.0
Matches 2; Conservative
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|:|:: 1 GFWNK 5

Corebellar degeneration-related protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: B35640
R;Chen, Y.T.; Rettig, W.J.; Yenamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner, J.B. Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990
A;Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal mark A;Reference number: A35640; MuID:90222173; PMID:2326268
A;Accession: B35640
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-6 <CHE>

43.6%; Score 17; DB 2; Length 6; 20.0%; Pred. No. 2.8e+05; ive 4; Mismatches 0; Indels 1; Conservative Query Match Best Local Similarity Matches 1; Conserv

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Gaps

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: |::: 1 FWEDL 5 2 YWXXX 6 ò 셤

RESULT 3 F41946

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Cyccossion: T13818
Cyccossion: T13818
Rybelatre, C.; Barrel, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A;Title: The main features of the craniate mitochondrial DNA between the ND1 and the COI A;Reference number: Z17775; MUID:97398704; PMID:9254918
A;Accession: T13818
A;Accession: T13818
A;Accession: T13818
A;Molecule type: DNA
A;Residues: 1-8 < DEL>
A;Molecule type: DNA
A;Cross-references: UNIPROT:021079; EMBL:Y09527; NID:g2340019; PIDN:CAA70718.1; PID:g2340; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pullulanase (BC 3.2.1.41) - Bacillus sp. (strain S-1) (fragment)
C;Species: Bacillus sp.
C;Species: Bacillus sp.
C;Daces: 19-May-1994 #text_change 03-Jun-2002
C;Accession: PN0649
R;Kim, C.H.; Choi, H.I.; Lee, D.S.
Biosci. Biochem, 57, 1632-1637, 1993
A;Title: Purification and biochemical properties of an alkaline pullulanase from alkaloph A;Reference number: PN0649; MUID:94080025; PMID:7764261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: PN0649
A;Molecule type: protein
A;Reducule type: protein
A;Reducule: 1-7 <KIM>
C;Comment: This enzyme is used togther with glucoamylase to improve the efficiency of stantent in high maltose syrups.
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T-cell receptor beta chain V-D-J region (161-2H) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0728
R;Peeney, A.J.
J; Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0509; MUID:91277601; PMID:1711558
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                                                                                                                       cytochrome oxidase subunit I - Atlantic hagfish mitochondrion (fragment) C;Species: mitochondrion Myxine glutinosa (Atlantic hagfish) C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
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A,Residues: 1-7 <PEB>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17; DB 2;
Pred. No. 2.8e+05;
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16.7%;
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Best Local Similarity 40.0%;
Matches 2; Conservative 5
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Best Local Similarity 16.7'
Matches 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: COI
C;Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Genome: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 WXXXWX 8
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2 YLSRWF 7
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                                                                                                  T13818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
30.2130
dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment)
C;Species: Phyllomedusa bicolor (two-colored leaf frog)
C;Species: Phyllomedusa bicolor (two-colored leaf frog)
C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 18-Aug-2000
C;Accession: S21230
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.
A;Tit.Le: Identification and characterization of two dermorphins from skin extracts of th A;Reference number: S21152; MUID:92339502; PMID:1633846
                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             act
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C.Species: Leucophaea maderae (Madeira cockroach)
C.Jate: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C.JAccession: JS0315
R.Holman, G.M.; Cook, B.J.; Nachman, R.J.
R.Holman, G.M.; Cook, E.J.; Nachman, R.J.
A.Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic A.Reference number: JS0315
T-cell receptor gamma chain (1a.27) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: F41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R. Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma (A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: F41946
A;Molecule typeliminary; not compared with conceptual translation
A;Residues: 1-6 cWHE>
C;Keywords: T-cell receptor
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C; Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile
C: Keywords: amidated carboxyl end; cephalomyotropic peptide
F; 8/ Modified site: amidated carboxyl end (Gly) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: S21230
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MIG>
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 6;
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16.7%;
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Best Local Similarity 16.7
Matches 1; Conservative
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A,Molecule type: protein
A,Residues: 1-8 <HOL>
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1 GSGFSSWG 8
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Matches 1; Conser
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FWYPN 7
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Biol. Chem. Hoppe-Seyler 373, 133-142, 1992
A;Title: Primary structures of neuropeptides isolated from the corpora cardiaca of varion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0221
R;Pamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
B;Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and jc
A;Reference number: PT0222; MUID:91108337; PMID:1899102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.) (fragmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RyFecency, A.J.
J. Exp. Med. 174, 115-124, 1991
A,Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A,Reference number: PT0509; MUID:91277601; PMID:1711558
A,Reference number: PT0580
A,Status: translation not shown
A,Molecule type: mRNA
A,Residues: 1-5 <FEE>
A,Experimental source: day 19 fetal thymus, strain BALB/c
C,Keywords: T-cell receptor
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0580
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Pred. No. 2.8e+05;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                  Length 8;
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Pred. No.: 2.8e+05;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)
                                                    ectrometry.
A;Reference number: S21663; MUID:92265187; PMID:1586453
                                                                                                                                                                                                                                               Score 16; DB 2; 1
Pred. No. 2.8e+05;
                                                                                                                                                                                                                                                                                                 4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Residues: 1-5 <YAM>
A,Experimental source: B lymphocyte
                                                                                             A,Accession: S21663
A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-8 <GAE>A,Cross-references: UNIPROT:P25423
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20.0%;
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Similarity 20.0%;
1; Conservative
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Best Local Similarity 20.0
Matches 1; Conservative
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Best Local Similarity
Matches 1; Conserv
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Matches 1; Conserv
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DENWS 5
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4 YSPDW 8
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Cispecies: Geotrupes stercorosus (dor beetle)
Cipate: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 09-Jul-2004
Cipate: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 09-Jul-2004
Cipate: 27-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 09-Jul-2004
Cipate: 27-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 09-Jul-2004
Rigade, G.
Biochem. J. 275, 671-677, 1991
A;Title: A unique charged tyrosine-containing member of the adipokinetic hormone/ red-pi
                                                                                                                                                                                                                                                                                                                C;Species: Melolontha melolontha (cockchafer)
C;Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 09-Jul-2004
C;Accession: S15422
C;Accession: S15422
B;Cochem. J. 275, 671-677, 1991
Biochem. J. 275, 671-677, 1991
A;Title: A unique charged tyrosine-containing member of the adipokinetic hormone/ red-pi A;Reference number: S15422; MUID:91248100; PMID:2039445
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C;Superfamily: adipokinetic hormone
C;Seywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
E;P;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental
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C;Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S21663
R;Gaede, G.; Lopata, A.; Kellner, R.; Rinehart, K.L.
                                                                        Gaps
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C.Superfamily: adipokinetic hormone
C.Superfamily: adipokinetic hormone
C.Superfamily: adipokinetic hormone
C.Superverdes: amidated carboxyl end, hormone; neuropeptide; pyroglutamic aci
F.1/Wodified site: pyrrolidone carboxylic acid (Gln) #status experimental
F.8/Modified site: amidated carboxyl end (Trp) #status experimental
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                          Length 7;
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                       Score 16; DB 2; I
Pred. No. 2.8e+05;
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20.0%; Pred. No. 2.8e+05;
tive 4; Mismatches 0;
     41.0%; Scc...
14.3%; Pred. No. ...
... 5; Mismatches
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S15422
adipokinetic hormone - cockchafer
                                                                      1; Conservative
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A;Molecule type: protein
A;Residues: 1-8 <BIO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein A; Residues: 1-8 <BIO>
                       Query Match
Best Local Similarity
Matches 1; Conserv
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1 FLNMSWF
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4 YSPDW 8
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C;Species: Gadus sp. (cod)
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 12-Jun-1998
C;Accession: S66195
R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C.
FEBS Lett. 367, 237-240, 1995
A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. February, A. 115-124, 1991
A. Tritle: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A. Fritle: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A. Reference number: PT0509; MUID:91277601; PMID:1711558
A. Reference number: PT0629
A. Status: translation not shown
A. Reperimental source: newborn thymus, strain BALB/c, clone 100-2AH
A. Reperimental source: newborn thymus, strain BALB/c, clone 100-2AH
A. Residus: translation not shown
A. Molecule type: mRNA
A. Residus: 1-6 -FEE2
A. Reperimental source: adult thymus, strain BALB/c, clone 100-4AB
C; Keywords: T-cell receptor
                                                                                                                                                                                                                                     A, Accession: S66195
A, Molecule type: protein
A, Residues: 1-6 (HDE)
C; Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C; Keywords: alcohol metabolism; NAD; oxidoreductase
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0629; PT0528
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38.5%; Score 15; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                 nzyme.
A;Reference number: S66191; MUID:95331382; PMID:7607314
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Best Local Similarity 20.0
Matches 1, Conservative
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Search completed: January 3, 2005, 17:36:16 Job time : 37 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

January 3, 2005, 17:26:09 Run on:

; Search time 188 Seconds (without alignments) 24.484 Million cell updates/sec

US-10-046-922-68 39 1 GYWXXXWX 8 score: Title: Perfect so Sequence: BLOSUM62DX Scoring table:

1825181 segs, 575374646 residues Searched:

835 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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16 4	1.0	•	OCES OCIMI	P58649 octopus min
16 4	1.0	4	EI01_LITRU	
16 4	1.0 7	8	Q9BRY4	Q9bry4 homo sapien
4	1.0	-1	AKH MELML	P25423 melolontha
4	•		COW2_CONPU	P58785 conus purpu
4	•	~	002831	002831 oryctolagus
	٠	-	LOKI_LOCMI	
m	8.5	-1	BRHP_CONIM	P58803 conus imper
m	8.5	-	TPFY_PACDA	P83455 pachymedusa
m	8.5	-	TYS1_LITRU	P82065 litoria rub
15 3	8.5	~	095945	
m	8.5	N	049223	glycin
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e	8.5	Н	AKH LIBAU	P25418 libellula a
15 3	8.5 8	Н		P61856 protophormi
15 3	s.	-	AKH_TABAT	595
15	8.5	٦	C125_CYPDO	P83661 cyphononyx

RESULT 2 AAB33374 SEQUENCE FROM N.A.
MEDLINE=95156893; PubMed=7853788;
Nakazato H., Hattori S., Ushijima T., Matsuura T., Koitabashi Y.,
Takada T., Yoshioka K., Endo F., Matsuda I.;
"Mutations in the COL4A5 gene in Alport syndrome: a possible mutation

AAB33374 PRELIMINARY; PRT; 8 AA.
AAB33374;
O2-MAR-2004 (TERMELrel. 27, Created)
O2-MAR-2004 (TERMELrel. 27, Last sequence update)
O2-MAR-2004 (TERMELrel. 27, Last annotation update)
Collagen alpha 5(IV) chain (Fragment).
Collagen (Human).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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P30369 P04549 P04549 P045410 P211140 P21142 P19989 P19989 P19989 P19989 P19989 P19989 P19989		e) a; Euteleostomi; ae; Murinae; Rat	, Friedman V., Dell'Orco R.T rat and human	† 4	6)
		ate) pdate pdate prate	A.I., 3.R., 1	CRC64;	~0
	TTS 8 AA.	eated) st sequence update) st annotation update) Craniata; Vertebrata; Sciurognathi; Muridae;	Roskams / , Jupe E	EFD3237B05A41376	w w
CN MACEU TO PERAM TO LEUMA CO	ALIGNMENTS	d) equer nnote iata; rogne	., RG .B., ion b	7805A	
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		01, 01, 08, 08, data ntia	=760 tewa , Da	168."; 11, ~. MW; 1	e de
	NARY;	• H 0	PubMed=7 C.M., Steins G.A.,	oding genes. 194 (1995). AAA86692.1; 8 8 8 A; 1150 MW;	33.3%; ative
######################################	PRELIMINARY	062721. 062721. 01-NOV-1996 (TrEMBLrel. 01-NOV-1998 (TrEMBLrel. Problibitin (Fragment). Rattus norvegicus (Rat) Bukaryota, Metazoa; Cho Mammalia; Eutheria; Rod MCBI_TAXID=10116;	SEQUENCE FROM N.A. STRAIN=Fisher; MEDLINE=9531633; PubMed=7607556; Altus M.S., Wood C.M., Stewart D.A., Roskams A.I Henderson T., Owens G.A., Danner D.B., Jupe E.R., McClung J.K.; "Regions of evolutionary conservation between the		Similarity 33. 2; Conservative WXXXWX 8 ::: : WRSEWK 7
155 155 155 155 155 155 155 155 155 155	Ħ.	062721; 01-NOV-1996 (TrEM 01-NOV-1998 (TrEM 01-NOV-1998 (TrEM Prohibitin (Fragm Rattus norvegicus Eukaryota; Metazo Mammalia; Eutheri NCBI TaxID=10116;	SEQUENCE FROM N.A STRAIN=Fisher; MEDLINE=9531633; Altus M.S., Wood Anderson T., Owe McClung J.K.; "Regions of evolu	prohibitin-endene 158:291-3 Gene 158:291-3 EMBL; U17178; NON TER SEQUENCE 8 2	al Sim: 2; 3 WXJ 2 WR8
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46.2%;
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NCBI_TaxID=6988;
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NCBI TaxID=6978;
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LCKS LEUMA
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                                                                                                                                                                                                                                                                                                                                 TISSUE-Fibroblast;
MEDLINE-95009907; PubMed=7523108;
MEDLINE-95009907; PubMed=7523108;
Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).
-I- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 6.6, its MW is: 19 kDa.

Direct protein sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Nucleotide sequences at the 5'-termini of the alfalfa mosaic virus RNAs and the intercristronic junction in RNA 3.";
Nucleic Acids Res. 8:5635-5647(1980).
EMBL; V00047; CAA23416.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=81124289; PubMed=6927843;
Koper-Zwarthoff B.C., Brederode F.T.M., Veeneman G., van Boom J.H.,
Bol J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alfalfa mosaic virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
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                                                                                                                                                                                                                   01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Unknown protein from 2D-PAGE of fibroblasts (P19) (Fragment).
                                                                 66.7%; Score 26; DB 2; Length 8; 33.3%; Pred. No. 1.8e+06; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.1%; Score 25; DB 1; Length 5; 40.0%; Pred. No. 1.8e+06; Live 3; Mismatches 0; Indels
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Last sequence update)
Last annotation update)
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                                             8 AA; 933 MW; 7370437735BAB378 CRC64;
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in primordial germ cells.";
Kidney Int. 46:1307-1314(1994).
EMBL; S75903; AAB33374.1; -.
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                                                                               Best Local Similarity 33.3
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WDSLWI 7
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P38639;
                                             SEQUENCE
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SEQUENCE
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TISSUE AND TOOK B.J., Nachman R.J.;

RA Holman G.M., Cook B.J., Nachman R.J.;

Holman G.M., Cook B.J., Nachman R.J.;

Holman G.M., Cook B.J., Nachman R.J.;

Tasolation, primary structure, and synthesis of leucokinins V and VI:

RT "Rolation, primary structure, and synthesis of leucokinins V and VI:

RT "Myotropic peptides of Leucophaea maderae.";

RL Comp. Biochem. Physiol. 88C:27-30(1987).

CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SUBCELLULAR LOCATION: Secreted.

DR PTR, JS0315; JS0315.

RAMIDATION: Direct protein sequencing; Neuropeptide.

RY Monidation; Direct protein sequencing; Neuropeptide.

FT MOD RES.

SEQÜENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;
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-!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Leucokinin V (L-V).
Leucophaea maderae (L-V).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Corpora cardiaca;
MEDLINE-98010462; PubMed=9350979;
Predel R., Kellner R., Rapus J., Penzlin H., Gade G.;
"Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Periplaneta americana (American cockroach).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Orthopteroidea, Dictyoptera, Blattaria, Blattoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.6%; Score 17; DB 1; Length 8; llarity 25.0%; Pred. No. 1.8e+06; Conservative 4; Mismatches 2; Indels
Score 18; DB 2; Length 8;
Pred. No. 1.8e+06;
3; Mismatches 1; Indela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Kinin-4 (Pee-K-4).
                                                                                                                                                                                                                                                                                                                                                                                        8 AA.
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-!- SUBCELLULAR LOCATION: Secreted.
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Query Match
Best Local Similarity
Matches 1; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                       3 WXXXWX 8
                                                                                                                                                                                                                                          1 WVAQYL 6
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SEQUENCE
                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                               Diadema.
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Q8W8G4;
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ID QE
AC QE
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                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion.
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Diadematacea; Diadematidae;
-!- MASS SPECTROMETRY: MW=838.15; METHOD=Electrospray; RANGE=1-8;
                                                                                                                                                                                                                                                                          Mitochondrion.
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
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                                                                     Similarity 25.0%; Pred. No. 1.8e+06; 2; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                              8 8 AA; 1129 MW; FOC7336411A04B56 CRC64;
                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Cytochrome oxidase subunit II (Fragment).
          NOTE-Ref.1.
--- SIMILARITY: Belongs to the kinin family.
Amidation; Direct protein sequencing; Neuropeptide.
MOD RES
SEQÜENCE 8 AA; 839 MW; 736365A5B9D6DDD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17; DB 2; 1
Pred. No. 1.8e+06;
                                                                                                                                                                                         8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diadema savignyi (Longspine black urchin).
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SEQUENCE FROM N.A.
MEDLINE=21323357; PubMed=11430656;
Lessios H.A., Kessing B.D., Pearse J.S.;
                                                                                                                                                                                                                                          Cytochrome oxidase subunit I (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Biol. Evol. 14:807-813(1997).
EMBL; Y09524; CAA70710.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
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Similarity 16.7%;
1; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                 1 GYWXXXWX 8
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GAQFSSWG 8
                                                                               Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7740;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion.
                                                                                                                                                                                                                                                                                                Branchiostoma
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SEQUENCE
                                                                         Query Match
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                                                                                                                                                                                                    Q7GEM6;
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Echinoidea, Euechinoidea, Diadematacea, Diadematoida, Diadematidae,
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"Population structure and speciation in tropical seas: global
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                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                          Score 17; DB 2; Length 8; Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                        701B173B46DDC2D3 CRC64;
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Last sequence update)
Last annotation update)
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8 AA; 1037 MW; 701B173B46DDC2D3 CRC64;
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                     urchin Diadema.";
                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytochrome oxidase subunit II (Fragment).
                                                                                                                                                                         EMBL; AY013102; ALL33868.1; -.
EMBL; AY013103; AAL33868.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
NAW TETAL
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GO; GO:0005739; C:mitochondrion; IEA.
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                                                     EMBL, AV013080; AAL33860.1; --
EMBL, AV013080; AAL33861.1; --
EMBL, AV013086; AAL33863.1; --
EMBL, AV013088; AAL33864.1; --
EMBL, AV013099; AAL33866.1; --
EMBL, AV013091; AAL33866.1; --
EMBL, AV013091; AAL33866.1; --
EMBL, AV013091; AAL33868.1; --
EMBL, AV013091; AAL33868.1; --
EMBL, AV013091; AAL33868.1; --
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16.7%;
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Similarity 16.7%;
1; Conservative
                     phylogeography of the sea ux
Evolution 55:955-975(2001).
EMBL; AX013065; AAL33860.1;
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                                                                                                                                                                                                                                                                                      8 AA; 1037 MW;
                                                                                                                                                                                                                                                                                                                                                                  1; Conservative
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Mitochondrion.
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Gaps

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Lessios H.A., Garrido M.J., Kessing B.D.;
"Demographic history of Diadema antillarum, a keystone herbivore on
Caribbean reefs.";
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Bukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Diadematacea; Diadematoida; Diadematidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21561594; PubMed=11703875;
Lessios H.A., Garrido M.J., Kessing B.D.;
"Demographic history of Diadema antillarum, a keystone herbivore on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21323357; PubMed=11430656;
Lessios H.A., Kessing B.D., Pearse J.S.;
"Population structure and speciation in tropical seas: global
phylogeography of the sea urchin Diadema.";
Evolution 55:955-975(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 16.7%; Pred. No. 1.8e+06; 1; Conservative 5; Mismatches 0; Indels
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                                                                                           Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).

EMBL; AY012796; AAL33821.1; -.

EMBL; AY012099; AAL3382.1; -.

EMBL; AY012804; AAL33823.1; -.

EMBL; AY012806; AAL33824.1; -.

EMBL; AY012806; AAL33826.1; -.

EMBL; AY012855, AAL33828.1; -.

EMBL; AY012857; C:mitochondrion; IEA.
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EMBL; AY012931; AAL33845.1; -.
EMBL; A00012922; AAL33846.1; -.
GO; GO:0001739; C:mitochondrion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                          701B173B46DDC2D3 CRC64;
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Last annotation update)
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8 AA; 1037 MW;
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SEQUENCE 8 AA; 1076 MW;
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Best Local Similarity 33.3.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Matches 1; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diadema mexicanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=105359;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caribbean reefs.";
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1 WVAQYL 6
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NON TER 1
SEQUENCE 8 AA
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OCP3_OCTMI
ID OCP3_OCTMI
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Q8W8G6
                      RRT RELEASE OF THE CONTROL OF THE CO
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                                                                                                                                                                           Mitochondrion.
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Diadematacea; Diadematoida; Diadematidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21561594; PubMed-11703875;
Lessios H.A., Garrido M.J., Kessing B.D.;
"Demographic history of Diadema antillarum, a keystone herbivore on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Diadematacea; Diadematoida; Diadematidae;
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                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21323357; PubMed=11430656;
Lessios H.A., Kessing B.D., Pearse J.S.;
"Population structure and speciation in tropical seas: global
phylogeography of the sea urchin Diadema.";
Evolution 55:955-975(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lessios H.A., Kessing B.D., Pearse J.S.;
"Population structure and speciation in tropical seas: global
phylogeography of the sea urchin Diadema.";
Evolution 55:955-975(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 17; DB 2; Length 8; Pred. No. 1.8e+06; 5; Mismatches 0; Indels
           01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit II (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR.2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit II (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 AA; 1037 MW; 701B173B46DDC2D3 CRC64;
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MEDLINE=21323357; PubMed=11430656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=21561594; PubMed=11703875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 43.6%;
Similarity 16.7%;
1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                       Diadema mexicanum.
                                                                                                                                                                                                                                                                                             NCBI_TaxID=105359;
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1 WVAQYL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitochondrion.
                                                                                                                          Name=COII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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TISSUBE-Ovary;

XX MEDINE-2238825;

XX Exausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Xx Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Xx Strausberg R.L., Feingold B.A.,

Xx Strausberg R.L., Feingold B.A.,

Xx Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Xx Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Xx Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Xx Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Xx Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Xx Raha S.S., Morley K.C., Hale S., Abramson R.D., Mullahy S.J.,

Xx Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Xx Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Xx Hilalon D.K., Muzny D.W., Sodergren B.D., Dickson R.S., Sanchez A.,

Xx Hilalon B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Xx Hilalon B., Young A.C., Shevchenko Y., Bouffard G.G.,

Xx Richards S.Y., Touchman J.W., Green B.D., Dickson M.C.,

Xx Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Xx Richards N.J., Marra M.A.,

Xx Generation and initial analysis of more than 15,000 full-length human
                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                               ol-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
805TM1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50030; UBA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Conservative
               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00165; UBA; 1.
SMART; SM00291; ZnF_ZZ;
                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
               Q9BRY4
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   Q9BRY4
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                                                                                                                                                                                       than Ocp-3.
--- SUBCELLULAR LOCATION: Secreted.
--- PIM: Ocp-4 has D-Ser instead of L-Ser.
--- PIM: Ocp-4 has D-Ser instead of L-Ser.
--- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                       Octopus minor (Octopus).

Bukaryota, Metazoa, Mollusca, Cephalopoda, Coleoidea, Neocoleoidea, Octopodiformes, Octopoda, Incirrata, Octopodidae, Octopus.

NCBI_TaxID=89766,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C., "Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae,
Pelodryadinae, Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
Amidation; Amphibian defense peptide; Direct protein sequencing.
MOD RES 6 Methionine amide.
SEQUENCE 6 AA; 792 MW; 6681704772C9A000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                     Score 16; DB 1; Length 4; Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16; DB 1; Length 6; Pred. No. 1.8e+06; 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                          D-amino acid; Direct protein sequencing; Hormone.
MOD_RES 2 2 D-serine (in form Ocp-4).
SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;
                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 41, Last sequence update)
(Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                      Cardioactive peptides Ocp-3/Ocp-4.
                                                                                                                                                            TISSUE=Brain;
MEDLINE=20336815; PubMed=10876044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Litoria rubella (Desert tree frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chem. 52:639-645(1999)
            28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last seq 05-JUL-2004 (Rel. 44, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                     41.0%;
50.0%;
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16.7%;
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Matches 2; Conservative
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Best Local Similarity
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FVPIWM 6
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05-JUL-2004
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                                                                                                                                                SEQUENCE
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ID EI01 L
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G0:0019901; F:protein kinase binding; ISS.
G0:0042169; F:SHZ domain binding; ISS.
G0:004130; F:ubiquitin binding; ISS.
G0:0015197; P:endosome transport; ISS.
G0:001542; P:intracellular signaling cascade; ISS.
G0:0045944; P:positive regulation of transcription from P. ..; ISS.
G0:0045944; P:protein localization; ISS.
G0:0043122; P:regulation of I-kappaB kinase/NF-kappaB cas. ..; ISS.
G0:0005950; P:response to stress; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.0%; Score 16; DB 2; Length 7; 66.7%; Pred. No. 1.8e+06; ive 0; Mismatches 1; Indels
Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  737728769DDDD6F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            completed: January 3, 2005, 17:35:33
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PROSITE; PS50135; ZF ZZ 2; 1.
SEQUENCE 7 AA; 779 MW; 737728769DI
                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000449; UBA.
InterPro; IPR000433; Znf_ZZ.
Pfam; PF00569; ZZ; 1.
                                                            EMBL; BC005857; AAH05857.3;
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Job time : 189 secs
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RESULT 15

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